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GenCore version 5.1.3
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OM nucleic - nu	 nucleic search, using sw model
Run on:	January 3, 2003, 20:11:57; Search time 7402 Seconds (without alignments) 11712.680 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-842-484A-1 2979 1 ttataaactgattaaagaagacatttgcattttattaaaa 2979
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	2054640 segs, 14551402878 residues
Total number of hits	f hits satisfying chosen parameters: 4109280
Minimum DB seq Maximum DB seq	length: 0 length: 2000000000
Post-processing:	g: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	<u>ធី</u> តិតិតិតិតិតិតិតិតិ
	24: en_pii:* 25: en pl:*

Pred. No. is the number of results predicted by chance to have a

em_htgo_other:* em_htgo_mus:* em_htgo_hum:*

fugurations 1 to 2979)
DeAngelis,P.L. and Padgett-McCue,A.J.
Identification and molecular cloning of a chondroitin synthase from Pasteurella multocida type F

Pasteurella multocida. Pasteurella multocida Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;

Pasteurella.

REFERENCE AUTHORS TITLE

BCT 07-AUG-2000

complete cds

AF195517 2979 bp DNA linear Pasteurella multocida chondroitin synthase CS gene,

GI:9716369

AF195517 AF195517.1

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AF195517

RESULT 1 AF195517 LOCUS DEFINITION

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em_co:*
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em_htg_rod:*

AC007926 Trypanoso AC116961 Dictyoste AC116965 Dictyoste AC116965 Dictyoste AF400048 Campyloba AV044866 Campyloba AV0786 V.cholerae AB012956 Vibrio ch AL51977 Listeria AL531280 Wuman DNA AC084152 Caenorhab AP003187 Clostridi Dictyoste Plasmodiu Dictyoste Dictyoste Dictyoste Sequence Sequence Campyloba Campyloba Streptoco Dictyoste Trypanoso Streptoco Plasmodiu Streptoco Plasmodiu Campyloba Dictyoste Pasteurel Pasteurel Escherich Nostoc sp Streptoco Campy loba Campyloba Pasteurel Pasteurel Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. AX413863 AX415777 AF401529 AF401528 AF343914 AB050723 AC116990 AC084397 AF349539 AL034556 AC114257 AC116923 AL034558 AC117080 AC116101 AC115600 AC005504 AF448502 AF215659 ALIGNMENTS SUMMARIES AX415777 AF401529 AF401528 AF343914 AB050723 AC116990 AC084397 AF349539 PFMAL3P5 AF003591 AF373595 AX009404 AF48502 AC005308 AE006155 CNS01804 AF130984 AF167344 AF036004 AF237926 AB079602 AL391280 AC084152 DB 100.0 88.5 88.6 88.6 88.6 88.6 188.6 Length Query Match 2635.8 2632.6 2340.8 2283.4 2268.6 Score Š

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/note="polysaccharide-forming glycosyltransferase; similar
to pasteurella multocida type A hyaluronan synthase"
/codon_start=1
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/db_xref="a[: 97170"
/db_xref="a[: 9717
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                                                                                                               Biochem. & Molec. Biol., Univ. of Oklahoma 940 Stanton L. Young Blvd., Oklahoma City,
                                                                                                                                                                                                                                                                    /country="USAS: Arkansas"/
/country="USAS: Arkansas"/
/note="capsule type F
isolated from face lesion of turkey from Arkansas; strain obtained from USDA"
61. 2958
/function="synthesizes the chondroitin polymer backbone polysaccharide composed of repeating disaccharide units polysaccharide composed of repeating disaccharide units polysaccharide of peta(1.4)plucuronic acid linked to beta(1.3)N-cetylgalactosamine) involved in capsule biosynthesis"
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/strain="P4679"
/db_xref="taxon:747"
                                                         2 (bases 1 to 2979)
DeAngelis, P. L. and Padgett-McCue, A.J.
Direct Submission
Submitted (15-OCT-1999) Biochem. & Mo
Health Sciences Center, 940 Stanton I
OK 73104, USA
  24124-24129
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Conservative 0; Mismatches
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AE006116 11885 bp DNA linear BCT 08-MAR-2001
Pasteurella multocida PM70 section 83 of 204 of the complete
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2 (bases 1 to 11885)

2 (bases 2 to 1885)

Direct Submission

Submitted (24-OCT-2000) Department of Veterinary Pathobiology,
University of Minnesota, 1971 Commonwealth Ave., St. Paul, MN
55108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pasteurella multocida.
Pasteurella multocida
Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;
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1 (bases 1 to 11885)
May, B.J., Zhang, Q., Li, L.L., Paustian, M.L., Whittam, T.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete genomic sequence of Pasteurella multocida, Pm70 Proc. Natl. Acad. Sci. U.S.A. 98 (6), 3460-3465 (2001) 21145866
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1. .11885
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AE006116 AE004439
AE006116.1 GI:12721075
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JOURNAL
MEDLINE
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10789. .11448
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Thomsond, K. M., Boyce, J.D., Chung, J.Y., Frost, A.J. and Adler, B. Direct Submission

Submitted (03-SEP-2000) Veterinary Pathology and Anatomy, The University of Queensland, School of Veterinary Science, Brisbane, QLD 4073, Australia

Location/Qualifiers
                                                                                                                                                                                                            Adler, B.
                                                                                                                             Pasteurellaceae;
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Loci
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Townsend, K.M., Boyce, J.D., Chung, J.Y., Frost, A.J. and Genetic organization of Pasteurella multocida cap Loci development of a multiplex capsular PCR typing system J. Clin. Microbiol. 39 (3), 924-929 (2001)
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S657

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AF067175 1000 16727 bp DNA linear BCT 05-MAY-2000 pasteurella multocida capsule biosynthesis gene cluster, complete
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2 (bases 1 to 16727)
Chung,J.Y., Zhang,Y. and Adler,B.
Direct Submission
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RQKDNGFQASAARNMGLRLAKYDFIGLLDCDMAPNPLWVHSYVAELLEDDDLTIIGPR
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VEKENSKKLENINQFLYFYKLGEITTIKTEDPPNTNNIVSHSWVNDTNTYLNAPLITI
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Submitted (19-MAY-1998) Microbiology, Monash University, Wellington Road, Clayton, VIC 3168, Australia 3 (bases I to 16727) Chang, J.Y., Zhang, Y. and Adler, B. Direct Submission Submitted (05-MAY-2000) Microbiology, Monash University, Wellington Road, Clayton, VIC 3168, Australia Sequence update by submitter on May 5, 2000 this sequence version replaced gi:3435183.
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GISALLHRMPVLTLGRASYNFEGLTYQGNLHSFWHNKGLPEAKVFEAYRKYHLSKTQI
NGSFYSKVILRYPYNQ"
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I SEGOKLWANDAPALLAWWINIGKOVANOVAOVOHEKELELSTIKERQLEVTEKVQLTEQ
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I KIDEAYHLTKKTLSDKEKALKTHQDEI EALKIIFNENI SVQEDMQEKFQETNKRKQE
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DFVVEKVNILDCINQVDEVHTMTSLAGFEALLREKKVHCYGLPFYSNWGLTVDHLSLN
RRSRKLSLLELIAGVLIYYPQYIDPKTKTMIDVQRAVDILIEQRRKIKNNKLHTNYFM
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complement(1157. .2383)
/gene="phyB"
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/gene="phyA"
/note="KpsS, LipA homolog"
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PKNQAALSGVGALLQSSGFARAQDDTYTVQEEMRSRSTLELLEKSIPIRQFYEDKGDL
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SYPNEPDLALEPYRLYNILATLFISLILYGITLLLLASIREHKN"
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                                                                                                                                         'note="BexC, CpxC homolog;
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                                                                                     /gene="hexc"
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TGGTACAAAAAGGGAAAGAATTTGGCATAAAACCTGAACATCAACATGTTGGTCTT
                                                                             TCTATTATCGTTACAACATTCAATCGACCAGCAATTTTATCGATTACATTAGCCTGTTTA
                                                                                                                                       7437 GACTTTATTGGCTTACTCGACTGTGATATGGCGCCAAATCCATTATGGGTTCATTAT
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                                          TCTATȚATTATTCCTACATTTAATCGTAGCCGTATTTTAGATATAACGTTAGCCTGTTTG
                                                                                                                   GTCAATCAGAAAACAAACTACCCATTTGAAGTCGTTGTTGCAGATGATGGTAGTAAGGAA
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Pasteurella.
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DeAngelis,P.L., Jing,W. and Achyuthan,A.M.
Direct Submission
Submitted (26-NOV-1997) Biochem. & Molec.
Health Sciences Center, 940 Stanton L. You
OK 73104, USA
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DeAngelis, P.L., Jing, W., Drake, R.R. and A. Identification and molecular cloning of a synthase from Pasteurella multocida J. Biol. Chem. 273 (14), 8454-8458 (1998) 98192645
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Fuller, T.E., Kennedy, M.J. and Lowery, D.E.
Direct Submission
Submitted (24-FEB-2000) Discovery Research, Pharmacia & Upjohn
Animal Health, 7923-25-434, 7000 Portage Road, Kalamazoo, MI
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Pasteurella multocida

Bacteria: Proteobacteria; gamma subdivision; Pasteurella.

Pasteurella.

I (bases 1 to 2919)

Fuller, T.E., Kennedy, M.J. and Lowery, D.E.
Identification of Pasteurella multocida virulence genes septicemic mouse model using signature-tagged mutagenesi.
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Best Local Sim:
Matches 2524;
RESULT 6
AF237926
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279 .	339	399	459	519 480	579	639	669	759	819 780	879 840	939	666	1059	1119	1179	1239	1299
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2y 2 0b 1	Oy 2 Db 2	Qy 3 Db 3	Oy 41	Oy 4 Db 4	Qy 5 Db 4	Oy 5 Db 5	Oy 6	Oy 7	Oy 7	Qy 8 Db 7	Qy 8 Db 8	Qy 9 Db 9	Qy 10 Db 9	Oy 10 Db 10	Oy 11 Db 10	Qy 11 Db 11	Oy 12 Db 13
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2y 13 0b 12 2y 13	0
	21 TIAGTITCAATTTATATCCCAGCTTATAACTGTGCAAACTATATTCAACGTTGCGTAGAT 13
77 77	420 AGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAATGGTTCGACG 1479
1,	480 GATAATACCTTAGAACTGATCAATAAGCTTATGGTAATAATCCTAGGGTACGCATCATG 1539
2y 1! 0b 1!	540 TCTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCCGTTTCTTTTGCTAAAGGT 1599
2y 16	AGTTGAACTGTGT 165
2y 16	660 TTAAAAGAATTTTTAAAAGATAAAAČGCTAGCTTGTGTTTATACCACTAATAGAAACGTC 1719
2y 1;	720 AATCCGGATGGTAGCTTAATCGCTAATGGTTACAATTGGCCAGAATTTTCACGAGAAAA 1777 -
Oy 17	780 CTCACAACGGCTATGATTGCTCACCATTT
2y 10	40 ACGGATGGATTAAACGAAAATATTGAAAACGCCGTGGATTATGACATGTTCCTTAAACTC 189
2y 15	900 AGTGAAGTTGGAAATTTAAACATCTTAATAAATCTGCTATAACCGCGTATTACATGGT 195
Oy 19	960 GATAACACA
2, YG	020 CAGTCATTAAATAGACAAGGCATCAATTAT
2y 2'	080 GAAAGTAGAAAGTATATCTTCAATAAAACC
2y 2;	140 AAAGATCTTAAACTCATTCAAAATAAAGATGC
Qy 2:	200 AATACATTAAACGGCTTAGTGAAAAAACTAAAC
2y 22 0b 22	260 TTCGTTATTATTCTACATGTTGATAAGAATCATCTTACACCAGACATCAAAAAGAAATA 231
2y 2 0b 2	320 TTGGCTTTCTATCATAAGCACCAAGTGAATATT
2	380 ACGAGTAATAGACTAATAAAAACTGAGGCACATTTAAGTAATATTAATAA

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Direct Submission
Submitted (07-FEB-2002) Nobuo Sugiura, Aichi Medical University,
Institute for Molecular Science of Medicine; 21, Yazako, Nagakute,
Aichi 480-1195, Japan (E-mail:nsugiura@aichi med-u.ac.jp,
UNLA http://www.aichi-med-u.ac.jp/imsm/index-e.html,
Tel 81-52-264-4811(ex.2087), Fax:81-561-63-3532)
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14483 bp DNA linear BCT 11-JUN-200 ESCARTICHIA COLI kpss, kfoF, kfoF, kfoT, kfoTs, kfoTs, kfoTs, kfoTs, kfoTs, kfoTs, kfoTs, kfoTs, kpsS hypothetical protein, predicted glycosyltransferase, UDP-glucose dehydrogenase, kfoE hypothetical protein, IS hypothetical protein, chondroitin polymerase, kfoB hypothetical protein, is hypothetical protein, chondroitin polymerase, kfoB hypothetical protein, depingrase, kfoB hypothetical protein, chondroitin polymerase, kfoB hypothetical protein, depingrase, kfoB hypothetical and complete cds.
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Molecular Cloning and Characterization of Chondroitin Polymerase
from Escherichia coli Strain K4
J. Biol. Chem. 277 (24), 21567-21575 (2002)
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Escherichia coli
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ninomiya, T., Suglura, N., Tawada, A., Sugimoto, K., Watanabe, H. and
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ENDL"
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                                                                                                                                                                                                                      RDIĀKKYSDTNFLCLRYFNPTGAHESGMIGESPĀDIPSNLVPYILQVĀMGKLĒKLMVF
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TFEKISGVRIPYEIVSRRDGDIAESWSSPEKANKYLNWKAKRELETMLEDAMRWQMKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 TAGCACTCAAATTATTTGAGAAGTCTGCTGAAACCTACGGGCGAAAAATCGTTGAATTCC 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 GAAAGAAAATGAATACATTATCACAAGCAATAAAAGCATATAACAGCAATGACTATGAAT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACCATTGTGCAAAAATACGAACAAAAACTTGACATAAAGTATGTAAGACAAAAAGATTA
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Pred. No. 8.2e-123;
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                                                                                                                                                                                                                                                                                                                                                                                       complement(13863. .14483)
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Best Local 9
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1 (bases 1 to 155204)
E1-Sayed, N.M., Ghedin, E., Song, J., Larkin, C., Wanless, D., Jones, K., Peterson, J., Hou, L., Zhao, H., Mason, T., Militscher, J., Pai, G., Van Aken, S., Utterback, T., Khalak, H.G., Gerard, C., Leech, V., Ullu, E., Melville, S., White, O., Adams, M.D., Donelson, J.E. and Fraser, C.M. Trypanosoma brucei GUTatlo.1 RPC193-3415 BAC genomic sequence
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El-Sayed, N.M., Khalak, H. and Adams, M.D.

El-Sayed, N.M., Khalak, H. and Adams, M.D.

Direct Submission

Submitted (28-JUN-1999) The Institute for Genomic Research, 971:

Medical Center Dr., Rockville, MD 20850, USA

On Jul 17, 2001 this sequence version replaced gi:12746529.

* NOTE: This is a 'working draft' sequence. It currently

* consists of I contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* This sequence as soon as it is available and

* the accession number will be preserved.
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1 (bases 1 to 100726)
2 (alcekner, G., Elchinger, L., Szafranski, K., Pachebat, J., Dear, P.,
Lehmann, R., Baumgart, C., Parra, G., April, J.F., Guigo, R., Kumpf, K.,
Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A. and
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                                                                    AC116961 100726 bp DNA linear HTG Dictyostelium discoideum chromosome 2 map 336856-437580 *** SEQUENCING IN PROGRESS ***, in ordered pieces.
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EVSSEA IRWNBRARKNGGGIGGGIGGGGIGGGIGGGIGGGIGGGIGGGAGABA
DGWLKSGCICPETPPCPVYTECPEPVVCNIAKIQIQINSTIKSLDECKKGKDGTNDNI
NVCKSHKDETQDWLTDCQKEYVKQTSHSSKDDTLISLRNCQAEYQKETFKKDKLCRGL
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                                                                                                                                  Direct Submission

Direct Submitted (21-MAY-2002) Genome Analysis, Institute of Molecular
Submitted (21-MAY-2002) Genome Analysis, Institute of Molecular
Biotechnology, Beutenberstr. 11, Jena 07745, Germany
CDS predictions from GeneID may contain errors. Further Information
is ayaliable from HMB Jena, Department of Genome Analysis
(http://genome.imb-jena.de/dictyostelium/)
and the Univerity Colonge, Institute for Blochemistry I
http://www.uni-koeln.de/dictyostelium/project.shtml
Funding
                                Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                Agency: Deutsche Forschungsgemeinschaft (DFG).
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
Location/Qualifiers
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/note="ORF_ID:dd_02644"
Direct Submission
Submitted (04-APR-2002) Genome Analysis, Institute o:
Biotechnology, Beutenberstr. 11, Jena 07745, Germany
3 (bases 1 to 100726)
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REFERENCE AUTHORS

KEYWORDS SOURCE

ACCESSION VERSION

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (18-MAY-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany CDS predictions from GeneID may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis
                                                                                                                                                                            AC116965 43993 bp DNA linear HTG 18-MAY-2002 Dictyostelium discoideum chromosome 2 map 497421-541412 strain AX4,
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

1 (bases 1 to 4399)
Gloeckner, G., Eichinger, L., Szafranski, K., Pachebat, J., Dear, P.,
Lehmann, R., Baumgart, C., Parra, G., April, J.F., Guigo, R., Kumpf, K.,
Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (04-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany 3 (bases 1 to 43993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agency: Deutsche Forschungsgemeinschaft (DFG).
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (http://genome.imb-jena.de/dictyostellium/)
and the Univerity Colonge, Institute for Blochemistry I
(http://www.uni-koeln.de/dictyostellum/project.shtml
Sequence and Analysis of Chromosome 2 of Dictyostelium
                                                                                                                                                                                                                                              *** SEQUENCING IN PROGRESS ***, in ordered pieces
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                                                                                                                                                                                                                                                                                                                                              HTG; HTGS_PHASE2.
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AUTHORS TITLE JOURNAL

TITLE REFERENCE

REMARK

AUTHORS TITLE JOURNAL

COMMENT

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acid synthase (neuBl), putative N-acetylglucosamine-6-phosphate 2-ephaerase (neuAl), CMP-NeuSAc synthetase (neuAl), putative acetyltransferase, and putative glycosyltransferase complete cds; and heptosyltransferase II (waaF) gene, partial cds.
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Michniewicz,J., Cunningham,A.M. and Wakarchuk,W.W.
The Genetic Bases for the Variation in the Lipo-oligosaccharide of
                                                                                                                                                                                                AF400048 llad2 bp DNA linear BCT 03-JAN-2 Campy-lobacter jejuni strain ATCC 43438 heptosyltransferase I (wa gene, partial cds; lipid A blosynthesis acyltransferase (htrB), putative two-domain glycosyltransferase, putative glycosyltransferase, beta-1.4-4-N-acetylghalactosaminyltransferase (cgtA), beta-1.3-galactosyltransferase (cgtA), beta-1.3-galactosyltransferase (cgtA), alpha-2.8-sialyltransferase (cgtII), putative sialic
Campylobacter jejuni
Bacteria; Proteobacteria;
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Submitted (15-JUL-2001) Institute for Biological Sciences, National
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Gilbert,M., Michniewicz,J., Karwaski,M.-F., Cunningham,A. and
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Glibert, M., Karwaski, M.F., Bernatchez, S., Young, N.M., Taboada, E., Michniewicz, J., Cunningham, A.M. and Wakarchuk, W.W.
The Genetic Bases for the Variation in the Lipo-oligosaccharide of the Mucosal Pathogen, Campylobacter jejuni. BIOSYNTHESIS OF SIALYLATED GANGLIOSIDE MIMICS IN THE CORE OLIGOSACCHARIDE J. Biol. Chem. 277 (1), 327-337 (2002)
                                                                                                                                                                                                                                                     Campylobacter jejuni
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sussex Drive, Ottawa, Ontario KlA
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Gilbert, M., Michniewicz, J., Karwaski, M.-F., Cunningham, A. and
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Submitted (10-JUL-2001) Institute for Biological Sciences,
Research Council of Canada, 100 Sussex Drive, Ottawa, Ontar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVVSSDSDEILNYAKSQNVDILKRPISLAQDDTTSDKVLLHALKFYKDYEDVVFLQPT
SPLRTNIHINEAFNLYKNSNANALISVSECDNKILKAFVCNDCGDLAGICNDEYPFMP
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                                                                                                                            EPLAAAIVGALNNILVAHIEGGEISGTIDDSLRHAISKLAHIHLVNDEFAKRRLMQLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MSLAIIPARGGSKGIKNKNLVLLNNKPLIYYTIKAALNAKSISK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11219 TAAAGATAATAGTTTAAATATGGTTTTAGAATTTGCTAAAAAAGATCCAAGGATAAAAAT 11160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11279 GCAAAGTTGTATAAATCAGACTTTAAAAGATATTGAAATTTTGATTATCGATGATAAAAG 11220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11159 CTTTCAAAATGAAGAAATTTAGGCACTTTTGCAAGTAGAAATTTGGGGGTTTTGCATTC 11100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1356 ACCTTTAGTTTCTATTTATATCCCCGCTTATAACTGTGCAAATTATTTCAAAGATGTGT 1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGATAGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGTTC 1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAGGTACCTTACATCTATAGAAAGCTTTTACCAATAGAAGATTCACATATTCATAGAAT 1355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative acetyltransferase"
/protein_id="AAK91729.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              variation in homopolymeric G-tract"
                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 82.4; DB 1;
Pred. No. 0.00037;
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9053. 0711
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/gene="neuA1"
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complement(5044. .5949)
/gene="cgtb"
complement(5044. .5949)
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HLGYDFFKQLKEFNAYFKFHEIYFNORITSGVYMCTVAIALGYKEIYLSGIDFYQNGS
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AFSKKDFKSYKNSFLAKIIYKISKIDQKFPWYKEIIKGSKTCNMSFFKTDFDKLDGFN
ENFIGWGREDSEFVARFLFNKGIFRRLKFKAIAYHIYHEENSKKMLESNHQIYLDIK
                                                                                                                                                                                                                                                                                                                                                                 KNVDVLWFDHDCTYEDNÍKNKHKKTRMEIFNPKEECIITPKEYANRALSVGSRDISFG
WNGMIDPNETKQIKKFINFIINDLHFGIILEASANKIYU-LGGKLLICKLRANSISN
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/db_xref="Gl:15430480"
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/product="putative
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/codon_start=1
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                                                                                                                                                                                       /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="cgtA"
4015. shr
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/gene="cgtA"
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/note="orf4"
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4015. .
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/db_xref="G1:15430486"

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kqeqvtidfarvlerperasvysikdikkgevlsmdniwvkrpglggisasefenilgkraldi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product-"putative N-acetylglucosamine-6-phosphate"
/protein_id="AAK96003.1"
/db_xref="GI:15430485"
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/product="putative sialic acid synthase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative acetyltransferase"
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51.7%; Pred. No. 0.00037;
tive 0; Mismatches 196;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             galactosyltransferase; mannose-1-phosphate guanylyl transferase; ORF21x9 gene; ORF34x7 gene; ORF35x9 gene; ORF30x2 gene; ORF40x0 gene; ORF40x1 gene; ORF41x3 gene; ORF41x8 gene; ORF50x8 gene; ORF50x8
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KMYAVWIVVNYRESYGMYACNGILFNHESPRRGETFVTRKITRGLANIAGGLEKCLYM
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EGGGVDEKGIVTAIEGDKAPALKVGDVVVQIDPRYFRPAEVETLLGDPSKAKQKLGWT
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Submitted (04-SEP-1996) P.A. Manning, University of Adelaide, Dept
of Microbiology and Immunology, GPO Box 498, Adelaide S A 5005,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
1 (bases 1 to 16265)
Manning, P.A.
                                          Revised by submittor 20-OCT-1996
2 (bases 1 to 16265)
2 Stroeher, U.H., Parasivam, G., Dredge, B.K. and Manning, P.A.
Novel Vibrio cholerae 0139 genes involved in lipopolysaccharide biosynthesis
   TAAAGGTTATTACATTGGGCAGTTAGATTCAGATGATTATCTTGAGCCTGATGCAGTTGA 1652
                                                                                                                                                                                                                                                                                                                                                                   16265 bp DNA linear BCT 3 V.cholerae ORF's involved in lipopolysaccharide synthese. 870786. 101.2244680
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STVETORFOTAAAMIYGLERSOIFFSYLVINITISEOERSIVTKSRARMIYKKOVLE
FYLLDVATTLLLÖWGOTASFELIVEDLYSAQILAFIANGMTLSGAIFSALESLSTOFYM
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2232. .3404
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ERKAINENERKNHPSDFDLYCVGWDFYFFSGSSIVRALNKPULLKWYNGYTIGERSPYS
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8852. 9865
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EQF"
9868. 10800
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164; Conservative
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Matches 164
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Yamasaki,S., Shimizu,T. and Hoshino,K.
Direct Submission
Submitted (14-APR-1998) Shinji Yamasaki, Internatinal Medical
Center of Japan, Research Institute; Toyama 1-21-1, Shinjuku, Tokyo
162-8655, Japan (E-mail:shinji@ri.imcj.go.jp, Tel:+81-3-3202-7181,
Fax:+81-3-3202-7354)
                                                                                                                                                                                                                                                                                                                                                                               vo/11 pp DNA linear BCT 16-OCT-1999 vibrio cholerae genes for O-antigen synthesis, strain MO45, complete cds. AB012956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamasaki,S., Shimizu,T., Hoshino,K., Ho,S.T., Shimada,T., Nair,G.B. Yamasaki,S., Shimizu,T., Hoshino,K., Ho,S.T., Shimada,T., Nair,G.B. and Takeda,Y.
The genes responsible for O-antigen synthesis of vibrio cholerae 013 are closely related to those of vibrio cholerae 02 gene 237 (2), 321-332 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio
                                                                                                                                                            TATGGTAATAATCCTAGGGTACGCATCATGTCTAAACCAAATGGCGGAATAGCCTCAGCA 1569
                                                                                                                                                                                              9014 ATGAAGAAGGATGACCTATTGTATTGGTTTCAAGAGAAAACAAAGGCTAATAGTAAGC 9073
                                                                                                                                                                                                                                           1570 ICAAATGCAGCCGTTTCTTTGCTAAAGGTTATTACATTGGGCAGTTAGATTCAGATGAT 1629
                                                                                                                                                                                                                                                                TGTGCAAATTATATTCAAAGATGTGTAGATAGTGCTCTTAATCAAACTGTTGTCGATCTC
                 GAGGTTTGTATTTGTAACGATGGTTCAACAGATAATACCTTAGAAGTGATCAATAAGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="probable LPS core synthesis"
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Location/Qualifiers
1. .46721
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LOCUS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="probable transport of capsular precursors"
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/note="probable regulation of O-antigen length"
/codon_start=1
/transl_table=11
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20961. .22079
                                                                                                                                                                    /transl_table=11
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/gene="wzz"
18485.
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19650. .2077
/gene="IS1358"
                                                                                      /note-"unknown"
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15645. 18380
/gene="wbfF"
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14935. .15525
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20961. .2207
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TDFGGTGLMOMPSARMLEEGELNILATTNNDDYLHYAISLQLFPWLETTVRTTQVHELL
SPQASFSGOTKYTDKSIDAKIRLMOESYWLPELSLGLRDIGGTGLEPGETLYATTQVHELL
SPQASFSGOTKYTDKSIDAKIRLMOESYWLPELSLGLRDIGGTGLEPGETLYATTQVH
ELL
SPLAPLAPLRAQLEDGENISSTDKISSTDGGRDSNYGGNGGMLDLGRMFTGGTALFGG
IEYQPTAPERQLEDGONDYRSDFPYTRGQPDAMPYTSPWNFGLTYALTDWADLRYS
YQRGYTLTAGLTFGTNLATLKPTWLDSPAPTYQPVPSKADLSDEWQRLSQDVANIAG
SPOEIYOGOSYVIKGSOYKYRDREGARHRAATLLANFGINRRYYRIIETSQDQPLT
EYQLNEAFKRIIDHDYPNARLSDAGHTDAATLLANFGINRRYYRIIETSQDQPLT
GGABDFYLYAIGVNANASYKMOHWQLSGTLYGNLIDNYDKFNYTVPPDGTNIKRVPT
LSRQYFEEPLRISHLQLLYFDRWQHFYTQAYAGYLETWFAGVGSELLYRPLGKNWAVG
                                                                                                                                                           TAYERTNODVIQULESFKFRATNALGSLGQBIDLDIDQRDTPWTVPSDVELSSAQLE
VDGKOFNAPYALMOSLNTSSEDKYSYSNLIRVDNYYLKLKGKEISPPSSPYWKFQHV
SRGTSSITSHLSAENILDGFNBEPPPTGICNDHNYTQLKTHTQKTDNTILELLID
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ETFLYQYQDLKKRTLGSELIDPSIDNIPLLKNISAQQDQQDLKRQPYTWWWLEE"
COMPLEMENT (10522. .12714)
                                                                             STFRFRQSDVPQNGYVSFVYSEGRDNFVSTYSKDFIPESFSIYAKNKNNNSNCLSIGS
GNNSNPQTSDYKSFIHIPDENKLFFFSLNHFNQLSFEPTNKLGRDVSVNSRRGRPLLL
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LLKVSAGRYLTĞDIGFTVDFSKQFASGVVAGAFATKTDLSAEEFGEGSFTKGFYISIP
LDLMTVRPSTERVNISWLPLQRDGGQMLSRQYGLYKMTDARSPWYERF"
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SLCVAAPLATSLEVRVAHNNQAIHSTRLSFSEPMRLDSAVMQTLEQAGLNTQQVEWPS
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WTRIAPQHNPRLNGSWLLTLNSKSTQVSVYGAVNQPGDVIWHNRLSAKDYAHAAGLID
EQISEIVVIQPDGIAQKHAVAYWNQDFNEVAPGAIVYVPLPLKRAFFDPTVTDADLNQ
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LNLDGANLISLESDSTDPLLLGLHRASIPREWHFYLSWQPGYHFRYLAHSQFITLGEQ
OKQLPNGESRTLLRIDEQITIAALNQQYHNQYWLEPSTGAVIASEQQLAPGTHRYALA
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    /translation="MHKPTISSVIALTLLGCGGGESGNSGNTTPPVKYFNVSFLDLDN
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/gene="wbfC"
complement(12711. .13577)
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complement(13577. .14266)
/gene="wbfD"
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/transl_table=11
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14390. .14638
/gene="orf6"
14390. .14638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALSYLY77 270050 bp DNA linear BCT 06-JUN-2002 Listeria monocytogenes strain EGD, complete genome, segment 5/12. ALS91977 ALS91824
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                                                                                                                                                                                                                                                                                                                                                                                                                  29788 ATGAAGAAGATGACGTATTGTATTGGTTTCAAGAGAAAACAAAGGGCTAATAGTAAGC 29847
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                                                                                                                                                                         29608 ATATAAGGTGGTTTTAAAATGAGTTCCCAAAAATATCGGTTGTTATGTTTATAAT 29667
                                                                                                                                                                                                                                                  1510 TATGGTAATAATCCTAGGGTACGCATCATGTCTAAACCAAATGGCGGAATAGCCTCAGCA 1569
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                                                                                                                                                                                                                        1390 TGTGCAAATTATATTCAAAGATGTGTAGATAGTGCTCTTAATCAAACTGTTGTCGATCTC 1449
                                                                                                                                                                                                                                                                                                       1450 GAGGTTTGTATTTGTAACGATGGTTCAACAGATAATACCTTAGAAGTGATCAATAAGCTT 1509
                                                                                                                                         1330 ATAGAAGATTCACATATTCATAGAATACCTTTAGTTTCTATTTATATCCCCGCTTATAAC 1389
                                                                                                                                                                                                                                                                                                                                   Listeria monocytogenes.
Listeria monocytogenes
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
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                                                            Length 46721;
/note="probable GDP-D-mannose dehydratase"
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E-mail: pglaser@pasteur.fr
Phone: +33 145 68 89 96, Fax: +33 (0)1 45 68 87

1. .270050
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                                                                                                      0; Mismatches 136;
                                                            Score 82.4; DB 1;
Pred. No. 0.00026;
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Glaser, P., Frangeul, L. and Rusnick, C.
Direct Submission
Discrete (106-JUN-2001) Glaser P., In:
Microorganismes Pathogenes, 25 rue du
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/db_xref="taxon:1639"
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56. .61
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69. .215
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                       /codon_start=1
                                                              2.8%;
54.7%;
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                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E. coli SugE protein (transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to E. coli SugE protein (transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1277. 1831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /ccdon_start=1
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2192. .2512
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1264. .1269
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426. .431
                                                                                                                                                                                                                                          /gene="lmo0851"
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                                                                                                                                                        LRLQ"
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//db_xref="G1:16410258" |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLEMGMNHRHEIEVLSKIAKPDIAIITNIGEAHIEYLGSREEIAKAKLEITAGLNPSG
ILIYPHEETLLLGNINGDFRQLTFGKSEAAEIYPLEIRAEBGGTSFITNWEPELEIFV
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LYGDAMKAGEVAESKIGGGKVHHFDTKESLETALLSEIKGNEWILVKGSYGMGLKDV
VENLIK"
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//db_xref="Brty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVNAMEWPQLVENSKQVLTEAKEVTLKNSPMFKRYQKKVTETPWTSTLQFKKMVALAK
PVFEHIEIPTFIAQGSADQVVPAEKSVNFLMESIPGPKELFILEGSKHVICQDEQADK
LESLALKTIPIGTGYAIWTGIGAVGSVTLGMIVFKERKSVGKLLFITMIIAGVVGLKL
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/gene="lmo0858"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
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     // (2650. 3774,3788. 3822)
/gene="ddlA"
2650. 2655
/gene="ddlA"
2662. 377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7788. .3822
/gene="ddla"
join(3822 .3828,3838. .5211)
3822. .3828
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/gene="lmo0857"
5263. .5268
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5998, .6036
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/gene="lmo0857"
5278, .soo
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5998. .6036
/gene="lmo0857"
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3838. 528
                                                                                                                                                                                                                                                                                                                                   2662. .3774
/gene="ddlA"
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WINGGAFWAVEFLIONKHQKIGFLGVYFSPSYEERLEGYKKALQYYHIPFNKYAIT
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FTVLSNPQLTTWCTNLSFWGERAVELMYNRIRKPDEGFVHLALATNLIARDSVGENKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 234478 ATTCTTTTGGAACCTTTAGTAAGTGTAATTATTCCAGTTTATAATGTAGAAAAGTATGTT 234537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 234652 CGAATTCGTTATTTGAAAAAGAAAATGCCGGACAAGCTACTGCCCGAAATTTGGATTA 234711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 234712 GATGTGGCTACGGGAGATTACATCGTGATGGTAGTGATGATTACATTAGCAAAAAC 234771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234597
                                                                                                                                                                                                                                                                                                                                                                                                                                   1345 ATTCATAGAATACCTTTAGTTTCTATTTATATCCCCGCTTATAACTGTGCAAATTATATT 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1405 CAAAGATGTGTAGATAGTGCTCTTAATCAAACTGTTGTTGTATTTGTATTTGT 1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGGTACGCATCATGTCTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCCGTT 1584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1585 TCTTTTGCTAAAGGTTATTACATTGGGCAGTTAGATTCAGATGATTATCTTGAGCCTGAT 1644
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 234538 AAACGATGCTTGGATTCAGTTCTTGAGCAAACATATCATAACCTCGAAGTTATCGTAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1465 AACGATGGTTCAACAGATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCCT
                                                                                                                                                                                                                                                                                                            Length 270050;
                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                            2.8%; Score 82.4; DB 1; Length 27 ilarity 55.0%; Pred. No. 0.00017; Conservative 0; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234772 CTAGTAGAAACTTGTTTGGATACTGTACAAAAAACGAA 234809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1645 GCAGTTGAACTGTTTTAAAAGAATTTTTAAAAGATAA 1682
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Plasmodium falcipa
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ABL32224
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 Pasteurella multocida.
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Listeria monocytog
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Copyright (c) 1993 - 2003 Compugen Ltd
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The present sequence is the coding sequence of the Pasteurella multocida chondroitan synthase PmCS. PmCS catalyses glycosaminoglycan polymerization to produce chondroitan: a linear polyacacharide which has viscoelastic properties which makes it useful for a number of applications. Chondroitan can be used with hyaluronic acid (HA) to coat medical devices e.g. catheters and sensors to reduce tissue abrasion. In addition, they can be used as bloadhesives for haemostatic sealing and healing of wounds and surgical incisions; and as biomaterials that provide sustained delivery of encapsulated drugs, to wounds, ulcers,
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                                                n method for the enzymatic transfer of sugar molecules to an ptor, useful for synthesis of e.g. polysaccharide bioadhesives delivery systems, including hybrid molecules
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        multocida chondroitin synthase. A chondroitin polysaccharide may be used as a hyaluronan polysaccharide substitute in medial or cosmetic applications, for example in eye or joint applications, for moisturiser or wound dressings. The enzyme may be used in covalently coupling specific drugs, proteins or toxins to the structurally modified procedures, covalently cross linking the hyaluronic acid itself or to other supports to achieve a gel or other three dimensional biomaterial
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                                                                                                                                                                                                                                                                                                  Chondroitin synthase; dermatan sulphate; chondroitin sulphate polymer; eye application; joint application; moisturiser; drug delivery; wound dressing; biocompatible film; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New chondroitin synthase gene obtained from Pasteurella multocida, useful as hyaluronan polysaccharide substitute in medial or cosmetic applications, e.g. for eye or joint applications, for moisturizer or wound dressings
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                                                                                                                                                                                                                                                                      Pasteurella multocida chondroitin synthase gene #1.
                                                                             Location/Qualifiers
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                                                              AATAGTATAACGCTATAAAACATTTGCATTTTATAAAA
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% q	1441	GTCGATCTCGAGGTTTGTATTTGTAACGATGGTTCAACAGATAATACCTTAGAAGTGATC	1500
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Oy Db	1801	CACCATTTAGAATGTTTACGATTAGAGCTTGGCATTTAACGGATGGAT	1860
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           CAAGTGAATATTTACTAAATAATGACATCTCATATTACACGAGTAATAGACTAATAAAA
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The present invention relates to the coding sequence of the Pasteurella multocida chondroitin synthase. A chondroitin polysaccharide may be used as a hyaluconan polysaccharide substitute in medial or cosmetic applications, for example in eye or joint applications, for moisturiser or wound dressings. The enzyme may be used in covalently coupling specific drugs, proteins or toxins to the structurally modified chondroitin for general or targeted drug delivery or radiological procedures, covalently cross linking the hyaluronic acid itself or to other supports to achieve a gel or other three dimensional biomaterial with stronger physical properties, and covalently linking hyaluronic acid to a surface to create a biocompatible film or monolayer. The present sequence is one version of the coding sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               New chondroitin synthase gene obtained from Pasteurella multocida, useful as hyaluronan polysaccharide substitute in medial or cosmetic applications, e.g. for eye or joint applications, for moisturizer or wound dressings
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yy do	781	TGCGATATGGCACCACAACAATTATGGGTTCATTCTTATCTTACAGAACTATTAGAAGAC 840 	
λά Q	841	AATGATATTGTTTTAATTGGACCTAGAAAATATGTGGATACTCATAATATTACGGCAGAA 900	
ka aa	901	CAATTCCTTAACGATCCATATTAATAGAATCACTACCTGAAACCGCTACAATAACAAT 960 	
oy Op	961 961	CCTTCGATTACATCAAAAGGAAATATGGTTGGATTGGAGATTAGAACATTTCAAAAAA 1020 	
Qy Db	1021 1021	ACCGATAATCTACGTCTATGTGATTCTCCGTTTCGTTATTTTGTTGCGGGTAATGTTGCA 1080	
Oy Dp	1081 1081	TTTTCTAAAGAATGGCTAAATAAAGTAGGTTGGTTCGATGAA 	
QY Dp	1141	GGCGAAGATGTAGAATTTGGTTACAGATTATTTGCCAAAGGCTGTTTTTTCAGAGTAATT 1200 	
Oy Db	1201	GACGGCGGAATGGCCATCCATCAAGAACCACCTGGTAAAGAAAATGAAACAGAACGGAA 1260 	
Qy Dp	1261 1261	GCTGGTAAAAGTATTACGCTTAAAATTGTGAAAGAAAAGGTACCTTACATCTATAGAAAG 1320 	
Qy Db	1321	CTTTACCAATAGAAGATTCACATATTCATAGAATACCTTTAGTTTCTATTATATCCCC 1380	
Qy Db	1381	GCTTATAACTGTGCAAATTATATTCAAAGATGTGTAGATAGTGCTCTTAATCAAACTGTT 1440 	
Oy Db	1441	GTCGATCTCGAGGTTTGTATTTGTAACGATGGTTCAACAGATAATACCTTAGAAGTGATC 1500 	
Q.y D.b		AATAAGCTTTATGGTAATAATCCTAGGGTACGCA 	

1561	agcatcaaatgcagccgtttcttttgctaaggttattacattgggcagttagat 162.
621 621	TCAGATGATTATCTTGAGCCTGATGCAGTTGAACTGTGTTTAAAAGAATTTTTAAAAGAT 1680
1681 1681	AAAACGCTAGCTTGTTTATACCACTAATAGAAACGTCAATCCGGATGGTAGCTTAATC 1740
1741	GCTAATGGTTACAATTGGCCAGAATTTTCACGAGAAAAACTCACAACGGCTATGATTGCT 1800
1801	CACCATTTTAGAATGTTTACGATTAGAGCTTGGCATTTAACGGATGGAT
1861 1861	
1921 1921	CATCTTAATAAAATCTGCTATAACCGGTATTACATGGTGATAACACATCCATTAACAAA 1980
1981 1981	CTCGGCATTCAAAAGAAAACCATTTTGTTGTTGTCAATCAGTCATTAAATAGACAAGGC 2040
2041	CAATTATATAATTATGAC
2101	TARARCCGCTGAATATCAAGAAGAAATGGATAT
2161	<u>a</u> – a
2221 2221	aaaaactaaacaatattattgaatataataaaaatatattggtattattgtgggggg
2281 2281	GATAAGAATCATCTTACACCAGACATC
2341 2341	CAAGTGAATATTTACTAAATAAT
2401	ACTGAGGCACATTTAAGTAATATTAATAATTAAGTCAGT
2461 2461	ATCATTTTGATAATCATGACAGCCTATTCGTTAAAAATGACAGC
2521 2521	AAATATGATGTCGCCATGAATTTCTCAGCATTAACACATGA
S CI	GCGCATCCACCATTAAAAAGCTGATTAAAACCTATTT77

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Query Match
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                                                                                       This DNA sequence codes for the hyaluronate synthase (pmHAS, see AAY06212) of Pasteurella multocida Carter Type A. The pmHAS enzym has different kinetic optime with respect to pH and metal ion dependence, and different Km values compared with the HAS enzymes of Streptococcus equisimilis (see AAY06206) and Streptococcus sorter and about 2 to 3 -fold lower for UDP sugars, and Vmax values are about 2 to 3 -fold higher. The invention provides recombinant vectors containing hyaluronate synthase DNA,
        AATGAACAAATTCAAAGTGCAAAAAAAGGCGAAAATATCCCCGTTAACAAGTTCATTATT
ATGAATGTGAAAGGGGCATCACAAGGTATGTTTATGAAGTATGCGCTACCGCATGAGCTT
                             AACACTGAGGATATTTGGTTCCAATTTGCACTTTTAATCTTAGAAAAGAAAACCGGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            , hyaluronate synthase for production of controlled molecular weight and targeting
                                                                                                                                                                                                                                                                       synthase; pmHAS; hyaluronic acid; hyaluronan;
                                                                                                                                                                                                                                                        Pasteurella multocida hyaluronate synthase pmHAS DNA
                                                                                                                                                            AATAGTATAACGCTATAAAACATTTGCATTTTATAAAA 2979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 123-125; 125pp; English
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19..2937
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97US-0064435.
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especially S. equisimilis hyaluronate synthase DNA (see AAX58841), and prokaryotic or eukaryotic host cells which produce the enzyme and its hyaluronic acid product, particularly a product with modified structure or molecular size. The hyaluronic acid produced this way is purer than that produced by conventional methods.
                                                                                                                                                                                                                                                                                                                                                                  43 ATTTTTAAAGGAAAGAAAATGAATACATTATCACAAGCAATAAAAGGCATATAACAGCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GCACATCTTTCTGTAAATAAAGAAGAAAAGTCAATGTTTGCGATAGTCCGTTAGATATT
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                                                                                                                                               DB 20; Length 2937
                                                                                                             Sequence 2937 BP; 1077 A; 482 C; 509 G; 869 T; 0 other;
                                                                                                                                               Score 2283.4;
                                                                                                                                                                   Pred. No. 0;
0; Mismatches
                                                                                                                                                 76.6%;
86.5%;
                                                                                                                                                                  Best Local Similarity 86.5
Matches 2540; Conservative
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	CAAAAAAACCGATAATCTACGTCTATGT 1041 	NTGTTGCATTTTCTAAAGAATGGCTAAAT 1101 	ntgggggggggggggggggggggggggggggggggggg	SAGTAATTGACGGGGAATGGCCATCCAT 1221	AACGCGAAGCTGGTAAAAGTATTACGCTT 1281 	YTAGAAAGCTTTTACCAATAGAAGATTCA 1341 	MINICCCGCTIATAACTGTGCAAATTAT 1401 	aaactgttgtcgatctcgaggtttgtatt 1461 	aagtgatcaataagctttatggtaataat 1521 	GGGGAATAGCCTCAGCATCAAATGCAGCC 1581 	agttagattcagatgattatcttgagcct 1641 	TAAAAGATAAAACGCTAGCTTGTTTAT 1701 	GCTTAATCGCTAATGGTTACAATTGGCCA 1761 	TGATTGCTCACCATTTTAGAATGTTTACG 1821 	ACGAAAATATTGAAAACGCCGTGGATTAT 1881 	AATITAAACAICITAATAAAATCIGCTAT 1941 	TTAAGAAACTCGGCATTCAAAAGAAAAC 2001 	GACAAGGCATCAATTATAAATTATGAC 2061
	2 AATATATCGTIGGATIGGAGATTAGAACATTICAAAAAAACCGATAATCTACGTCTATGT 	2 GATTCTCCGTTTCGTTATTTTGTTGCGGGTAATGTTGCTGCATTTTCTAAAGAATGGCTAAAT	2 AAAGTAGGTTGGTTCGATGAAGAATTTAATCATTGGGGGGGG	2 TACAGATTATTGCCAAAGGCTGTTTTTCAGAGTAATTGACGGCGGAATGGCCATCCAT	2 CAAGAACCACCTGGTAAAGAAAATGAAACAGAACGCGAAGCTGGTAAAAGTATTACGCTT 	2 AAAATTGTGAAAGAAAGGTACCTTACATCTATAGAAAGCTTTTACCAATAGAAGATTCA 	2 CATATTCATAGAATACCTTTAGTTTCTATTATATCCCGGCTTATAACTGTGCAAATTAT 	2 ATTCAAAGATGTGTAGATAGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATT	2 TGTAACGATGGTTCAACAGATAATACCTTAGAAGTGATCAATAAGGCTTTATGGTAATAAT 	2 CCTAGGGTACGCATCATGTCTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCACCC 	GITICTITIGCTAAAGGITATIACAIIGGGCAGITAGAIICCAGAIGAITAICIIGAGCCT	2 GATGCAGTTGAACTGTGTTTAAAAGAATTTTTAAAAGATAAAACGCTAGCTTGTGTTTAT 	ACCACTAATAGAAACGTCAATCCGGATGGTAGCTTAATCGCTAATGGTTACAATTGGCCA	22 GAATTITCACGAGAAAACTCACAAGGCTATGATTGCTCACCATTITAGAATGTTTAGG 	22 ATTAGAGCTTGGCATTTAACGGATGGATTTAACGAAAATATTGAAAACGCGGGGGTTAT 	12 GACATGTTCCTTAAACTCAGTGAAGTTGGAAATTTAAACATCTTAATAAAATCTGCTAT 	12 AACCGCGTATTACATGGTGATAACACATCCATTAAGAAACTCGGCATTCAAAGAAAAAC 	02 CATTTTGTTGTAGTCAATCAGTCATTAAATAGACAAGGCATCAATTATTATAATTATGAC
901	982	1042	1102	1162	1222	1282	1342	1402	1462	1522	1582	1642	1702	1762	1822	. 1882	1942	2002
q	Qy	Qy	Qy	Qy Dp	Qy	Oy Dp	Qy Db	Qy Dp	QY	Qy	Qy Dp	Qy Db	Qy Dp	Qy	Qy Db	Qy	Qy Db	δy

2241 2460 CIGACITATATGCCIIGGGAACGAAATIACAAIGGACAAAIGAACAAAITCAAAGIGCA 2901 2181 2160 2361 2340 2400 2481 2521 TTCTCAGCATTAACACATGATTGGATCGAGAAAATCAATGCGCATCCACCATTAAAAG 2580 CAAGGTATGTTTATGAAGTATGCGCTACCGCATGAGCTTCTGACGATTATTAAAGAAGTC 2721 2641 CAAGGTATGTTTATGAGGTATGCGCTAGGGCTTCTGACGATTATAAGAAGTC 2700 ATCACATCCTGCCAATTGATAGTGTGCCAGAATATAACACTGAGGATATTTGGTTC 2781 CAATTTGCACTTTTAATCTTAGAAAAGAAAACCGGCCATGTATTTAATAAAACATCGACC 2841 2301 2421 TTCTCAGCATTAACACATGATTGGATCGAGAAAATCAATGCGCATCCACCATTTAAAAAG 2601 CATTITGITGIAGICAAICAGICATIAAAIAGACAAGGCAIAACITAITAIAAITAIGAC 2040 ATTAATAAATTAAGTCAGTTAAATCTAAATTGTGAATACATCATTTTTGATAATCATGAC 2401 ATTAATAAATTAAGTCAGTTAAATCTAAATTGTGAATACATCATTTTGATAATCATGAC 2161 GTCAGTATTTTTTATCCCAATACATTAAACGGCTTAGTGAAAAAACTAAACAATATTTT GAATATAATAAAAATATATTCGTTATTATTCTACATGTTGATAAGAATCATCTTACACCA 2221 GAATATAATAAATATATTCGTTATTGTTCTACATGTTGATAAGAATCATCTTACACCA 2302 GACATCAAAAAAGAAATATTGGCTTTCTATCATAAGCACCAAGTGAATATTTACTAAAT multocida hyaluronate synthase (PmHAS) nucleotide sequence BP 2937 (first entry) AAZ35589 standard; DNA; 01-FEB-2000 AAZ35589; 2761 2842 2902 2542 2662 2722 2701 2782 2821 2881 2422 1981 2122 2101 2182 2242 RESULT 5 AAZ35589 X E X E X E X E X g ΩD q Dβ g οy δy δ g qq g δy g δ qq QY qq δy Dp Qγ g Qγ ò q g δŽ QΥ ò QΥ ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated hyaluronate synthase nucleic acids, used for the production of hyaluronic acid, for developing antibiotics and vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 GCAACACGCTCTTACTTTCCAACGTAAAAATTAACTCTATCCGAATCAGAAAAAAC 321
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uyaluronate synthase; PmHAS; hyaluronan; hyaluronic acid; HA;
drug dellvery; anglogenesis; wound healing; capsule synthesis;
fowl cholera; shipping fever; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2283.4; DB 21; Length Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be used as vaccines for fowl cholera or shipping fever.
                                                                                                                                                                                    "Hyaluronate synthase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 113-114; 121pp; English.
                                                                                                            Location/Qualifiers
19.2937
/*tag a /product= PmHAS /note= "Hyaluronate s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and for diagnostic applications
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86.5%;
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tissue abrasion; viscoelastic replacement;
bloadhesive; ss.
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cataract; arthritis; ulcer;
hyaluronic acid production;
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99US-0283402.
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01-APR-1999;
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The present sequence is the coding sequence of the soluble recombinant form of Pasteurealla multocida hyaluronic acid synthase-D, PmHAS-D. This sequence encodes residues I to 703 of the 972 residues of the native PmHAS enzyme. PmHAS-D catalyses glycosaminoglycan polymerisation to produce hyaluronic acid, HA: a linear polysaccharide. HA has viscoelastic produce hyaluronic acid, HA: a linear polysaccharide. HA has viscoelastic consections which makes it useful for a number of applications. HA can be used during ophthalmic surgery as a viscoelastic replacement for the vitreous humour e.g. during implantation of intraocular lenses in cataract patients. HA nijections directly into joints is also used to alleviate pain associated with arthritis. HA can also be used to cat medical devices e.g. catheters and sensors to reduce tissue abrasion. HA can also be used as bioadhesives for haemostatic sealing and healing of wounds and surgical incisions; and as biomaterials that provide sustained delivery of encapsulated durys, to wounds, ulcers, injuries or surgical sites. The present sequence can therefore be used to produce HA.
        or
  polysaccharide bioadhesives
                            drug delivery systems, including hybrid molecules
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  synthesis
  acceptor, useful for
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Sequence 2112 BP; 745 A; 359 C; 387 G; 621 T; 0 other;

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	5%; Pred. No. 2.8e-281; 0; Mismatches 348; Indels 21;	ATGAATACATTATCACAAGCAATAAAAGCATATAACAGCAATGACTATGAATTAGCACTC 120	ATGAATACATTATCACAAGCAATAAAAGCATATAACAGCAATGACTATCAATTAGCACTC 60	AAATTATTGAGAAGTCTGCTGAAACCTACGGCGAAAAATCGTTGAATTCCAAATTATC 180	GAAATCTATGGACG	CTCGACCAATTCTTATGTAAGT 219	AAATGCCAAGAAAAACTCTCAGCACATCTTCTGTTAATTCAGCACATCTTTCTGTAAAT 180	GAAGATAAAAAAAACAGTGTTTGCGATAGCTCATTAGATATCGCAACACAGCTCTTACTT 279	AAAGAAAAAAGTCAATGTTTGCGATAGTCCGTTAGATATTGCAACACACAC	TCCAACGTAAAAAATTAACTCTATCCGAATCAGAAAAAAAA	AGTACTTTCTGACTCGGAAAAACACGTTAAAAAATAAATGG 300	AAATCTATCACTGGGAAAAAATCGGAGAACGCAGAAATCAGAAAGGTGGAACTAGTACCC 399	GAAATCTGAAAATGCGGAGGTAAGAGCGGTCGCCCTTGTACCA 360	AAAGATTTTCCTAAAGATCTTGTTCTTGCTCCATTGCCAGATCATGTTAATGATTTTACA 459	TCTGGTTTTAGCGCCTTTACCTGATCATGTTTACA 420	TGGTACAAAAATCGAAAAAAAGCTTAGGTATAAAGCCTGTAAATAAGAATATCGGTCTT 519	GAAAAGACTIGGCATAAAACCTGAACATCAACATGTTGGTCTT 480	ICTATTATTATTCTACATTTAATCGTAGCCGTATTTTAGATATAACGTTAGCCTGTTTG 579	TCTATTATCGTTACAACATTCAATCGACCAGCAATTTTATCGATTACATTAGCCTGTTTA 540	GTCAATCAGAAACAAACTACCCATTTGAAGTCGTTGTTGCAGATGATGGTAGGAA 639	GTAAACCAAAAAACACATTACCCGTTTGAAGTTATCGTGACGAGATGATGGTAGTCAGGAA 600	AACTTACTTACCATGTGCAAAAATACGAACAAAAACTTGACATAAAGTATGTAAGACAA 699	GATCTATCACCGATCATTCGCCAATATGAAAATAGATATTCGCTACGTACG	AAAGATTATGGATATCAATTGTGTGCAGAAACTTAGGTTTACGTACAGCAAAGTAT 759
Match	Similarity 3; Conservat		1 ATGAATACATTATCACA						-															
Ouerv	Best Lo	0у 61	Db 1	0y 121	DP 61	Qy 181	Db 121	Qy 220	Db 181	Qy 280	Db 241	Оу 340	301	Ολ 400	19E qa	Qy 460	Db 421	Qy 520	Db 481	Qy 580	Db 541	Qy 640	Db 601	Qy 700

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AAAGATAACGGTTTTCAAGCCAGTGCCGCTCGGAATATGGGATTACGCTTAGCAAAATAT
                   GATTTTGTCTCGATTCTAGACTGCGATATGGCACCACAACAATTATGGGTTCATTCTTAT
                            GTTGCAGAGCTATTAGAAGATGATTTAACAATCATTGGTCCAAGAAAATACATCGAT
                                                                                                                  ACACAACATATTGACCCAAAAGACTTCTTAAATAACGCGAGTTTGCTTGAATCATTACCA
                                                                                                                                                                              AGATTAGAACATTTCAAAAAACCGATAATCTACGTCTATGTGATTCTCCGTTATAT
                                                                                                                                                                                                                      TTAGTTTCTATTTATATCCCCGCTTATAACTGTGCAAATTATATTCAAAGATGTGTGTAGAT
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                                                                                                ACTCATAATATTACCGCAGAACAATTCCTTAACGATCCATATTTAATAGAATCACTACCT
                                                                                                                                      GAAACCGCTACAAATAACAATCCTTCGATTACATCAAAAGGAAATATATCGTTGGATTGG
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A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAX12938 to AAX13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to
                                                                                                                                   1980
                                                                                                                                                                                                                ACGGATGGATTTAACGAAAATATTGAAAACGCCGTGGATTATGACATGTTCCTTAAACTC 1899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                       GATAACACATCCATTAAGAAACTCGGCATTCAAAAGAAAAACATTTTGTTGTAGTCAAT
                                                                                                                                                              CAGTCATTAAATAGACAAGGCATCAATTATTATAATTATGACAAATTTGATGATTTAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
                                                      AGTGAAGTTGGAAAATTTAAAACATCTTAATAAAATCTGCTATAACCGCGTATTACATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterococcus faecalis genome contig SEQ ID NO:137
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97US-0044031.
97US-0046655.
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2101 AAAGATATTTAA 2112
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06-MAY-1997;
16-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                   modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                1354 ATACCTTTAGTTTCTATTTATATCCCCGCTTATAACTGTGCAAATTATATTCAAAGATGT 1413
                                                                                                                                                                                          1001 ATGCCCAAAATTAGTATTATTGTTCCTGTATACAATGTAGAAAAATATTTAGAAAAATGT 1060
                                                                                                                                                                                                                       GTAGATAGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGT 1473
                                                                                                                                                                                                                                                1474 TCAACAGATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCCTAGGGTACGC 1533
                                                                                                                                                                                                                                                                                                                                                                                          1594 AAAGGTTATTACATTGGGCAGTTAGATTCAGATGATTATCTTGAGCCTGATGCAGTTGAA 1653
                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides, antibodies and modulators
                                                                                                                                                                                                                                                                                                    1121 retecadacaditergadeadeardergreatearirgergaacaagarcaacgggraaa
                                                                                                                                                                                                                                                                                                                                   ATCATGTCTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCCGTTTCTTTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibacterial; Listeria; food contamination; mutational analysis;
                                                                                                                                        ;
0
                                                                                                             Length 5550;
                                                                              Sequence 5550 BP; 1940 A; 806 C; 1041 G; 1763 T; 0 other;
                                                                                                                                        Indels
                                                                                                                                       0; Mismatches 150;
                                                                                                           Score 86; DB 20;
Pred. No. 2.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Listeria monocytogenes EGD DNA sequence #165
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1654 CIGIGITIAAAAGAATITITAAAAGA 1679
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ilarity 54.0%;
Conservative
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                                                                                                                           Best Local Similarity
Matches 176; Conserv
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(CNRS ) CNRS
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                                                           infection
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                                                                                                                Query Match
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The present invention relates to nucleic acid sequences (ABG67188-ABG71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in anti-Listeria vaccines.
                                                                                                                                                                                                                                  1356 ACCTITAGITICIATITAFATCCCCGCTTATAACTGTGCAAATTATATTCAAAGATGTGT 1415
                                                                                                                                                                                                                                                                                   1416 AGATAGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGTTC 1475
                                                                                                                                                                                                                                                                                                                                   AACAGATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCCTAGGGTACGCAT 1535
                                                                                                                                                                                                                                                                                                                                                                                   CATGTCTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCCGTTTCTTTTGCTAA 1595
                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGTȚATTACATTGGGCAGTTAGATTCAGATGATTATCTTGAGCCTGATGCAGTTGAACT 1655
                                                                                                                                                                                                                                                                                                  126 GACTGATAATTCAGCTAAAGTCATAAAAGTTATCTCAGATAA-----TCGAATTCGTTA 179
                                                                                                                                                                                                                                                                                                                                                                                                          180 TTTTGAAAAGAAAATGGCGGACAAGCTACTGCCCGAAATTTTGGATTAGATGTGGCTAC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 GGGAĞATTACATCGTGATGGTAGATAGTGATTACATTAGCAAAAACCTAGTAGAAAC 299
                                                                                                                                                                                                                                                           65
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                  a; food contamination; mutational analysis;
                                                                                                                        of the printed specification, but was obtained in electronic fo directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                             ;
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                                                                                                                                                                                     Length 984;
                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electror
                                                                                                                                                                                2.7%; Score 81; DB 24; Length 98
55.4%; Pred. No. 1.7e-06;
ive 0; Mismatches 140; Indels
                                                                                                                                                           Sequence 984 BP; 360 A; 136 C; 190 G; 298 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA sequence #167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1656 GTGTTTAAAAGAATTTTTAAAAGATAA 1682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABQ69955 standard; DNA; 984
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                                                                                                                                                                                                           Matches 181; Conservative
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                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1356 ACCTTTAGTTTCTATTTATATCCCCGCTTATAACTGTGCAAATTATATTCAAAGATGTG 1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1416 AGATAGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGTTC 1475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1536 CATGTCTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCCGTTTCTTTTGCTAA 1595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 GGGAGATTACATCGTGATGGTAGATAGTGATGATTACATTAGCAAAAACCTAGTAGAAAC 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 ACCITIAGIAAGIGIAATIATICCAGITIATAATGIAGAAAAGIAIGITAAACGAIGCIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection,
treatment and prevention of infection, also related polypeptides, antibodies and modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding enzymes involved in exopolysaccharide biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the printed specification, but was obtained in electronic for directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 984;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 984 BP; 360 A; 136 C; 190 G; 298 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.7%; Score 81; DB 24;
55.4%; Pred. No. 1.7e-06;
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                                                                                                                                                                           Claim 16; SEQ ID 2768; 180pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 TIGITIGGATACTGTACAAAAACGAA 326
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/product= "EPS1"
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-MAR-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-ESDB; AAYS4065, AAX54066, AAX54067, AAX54068, AAY54069, AAY54070.
AAX54071; AAX54072, AAX54073, AAX54074.
                                                                                                                                                                                   /note= "encodes AAY54070; contains 1 stop codon at nucleotides 9410-9412"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant enzymes for synthesis of exopolysaccharides, particularly in lactic acid bacteria, for improving properties fermented milk products
                                                                                                                                                                                                                                                                                               /product= "EPS9"
/note= "encodes AAY54073"
16919..18016
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.2838..13788
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14138..15553
                                                                                                                                                 note= "encodes AAY54069"
633..10681
  "encodes AAY54065'
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..4822
                                                                                                             note= "encodes AAY54068
                                                                         "encodes AAY54067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Germond JE, Lamothe G;
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/product= "EPS10"
                                                                                                                                                                                                                                                              'product= "EPS8"
                                                                                                                                                                                                                          "EPS7"
                                                                'product= "EPS3"
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                                                                                                                                         "EPS5"
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                             product= "EPS2"
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98EP-0201312.
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22-APR-1998;
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unit, present at the end of a chain of sugar residues bonded to the primer. EpS1 to EpS4 are used to elongate the EPS chain, and to regulate EPS production, BPS5 creates new bonds between saccharides, EPS6 is used in the biosynthesis of EPS, and EPS9 and EPS9 are beta-glycosyltransferases, EPS9 is a transporter of repetitive units, and EPS10 catalyses the conversion of a pyranose form of a beta-1-galactose to the furanose form. The EPS enzyme are used to improve properties of foods, particularly fermented milk products such as yoghurt and cheese, e.g. their organoleptic properties and flavour stability.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19966 BP; 6405 A; 3134 C; 3732 G; 6694 T; 1 other;
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/product= "eps1"
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3390..4121
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Best Local Similarity 52.0
Matches 179; Conservative
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12914 TAGCTCAAACATATCGCAATATTGAAGTCATTATAGTAAATGATGGTAGCACAGATCAGT 12973
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                                                                                                                                                                                                                12794 ACTGTTAGAATATGATTTTATATAATTAGGAGTAGAATAAAGAGAGATGAATCCATTAATAT 12853
                                                                                                                                                                                                                                                                                                                                                                                                          CCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCCTAGGGTACGCATCATGTCTAAAC 1546
                                                                                                                                                                                                                                                                                                                                 1427 TTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGTTCAACAGATAATA 1486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1547 CAAATGGCGGAATAGCCTCAGCATCAAATGCAGCCGTTTCTTTTGCTAAAGGTTATTACA 1606
                                                                                                                                                                         1307 ACATCTATAGAAAGCTTTTACCAATAGAAGATTCACATATTCATAGAATACCTTTAGTTT 1366
                                                                                                                                                                                                                                                    1367 CTATTTATATCCCCGCTTATAACTGTGCAAATTATTCAAAGATGTGTAGATAGTGCTC 1426
a free-flowing character and/or a smooth, creamy texture to acidified milk products (yoghurt or cheese).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acetyltransferase; glycosyltransferase; Beta-1,4-GalNAc transferase;
Beta-1,3-galactosyltransferase; alpha-2,3-sialyltransferase;
sialic acid synthase; CMP-sialic acid synthetase; mimic; antibody;
                                                                                                 Length 19966;
                                                          Sequence 19966 BP; 6405 A; 3133 C; 3732 G; 6695 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= Beta 1,2- galactosyltransferase/note= "Open reading frame 6a"
                                                                                                                   Pred. No. 4.1e-06;
0; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biosynthetic locus; biosynthesis; lipid A biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1607 TTGGGCAGTTAGATTCAGATGATTATCTTGAGCCTGATGCAGTT 1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= Beta 1,4-GalNAc transferase
/note= "Open reading frame 5a"
                                                                                               DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transferase
o frame 3a"
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1234..2490
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                                                                                               Score 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunity; immunogen; ganglioside; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 350..1237
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                                                                                               2.78;
52.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Campylobacter jejuni OH4384
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                                                                                                                   Best Local Similarity 52.0
Matches 179; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA53720;
                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                            1487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant enzymes for biosynthesis of exopolysaccharides having e.g. antitumor or probiotic properties or useful in fermented milk products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "encodes AAV43776; this CDS, minus the termination codon, is specifically claimed (claim 6)"
                                                                                                                                                                   /product "eps6; this CDS, minus the termination codon, is specifically claimed (claim 6)" /note "encodes AAY43772; contains a stop codon at nucleotides 9410-9412"
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                                                                                                                                                                                                                                                                                                     /note= "encodes AAY43773; this CDS, minus the termination codon, is specifically claimed (claim 6)"
                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "encodes AAY43774; this CDS, minus the termination codon, is specifically claimed (claim 6)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "encodes AAY43775; this CDS is specifically claimed (claim 6)"
                                                                                                               note= "encodes AAY43771"
633..10681
                                        "encodes AAY43770"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-013255/01.
P-PSDB; AAY43767, AAY43768, AAY43769, AAY43776.
AAY43773, AAX43774, AAX43775, AAX43776.
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/product= "eps10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "eps9"
                    "eps4"
                                                                                               "eps5"
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                                                                                                                                                                                                                                                    ..11671
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98EP-0201312.
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                                        'note= "enc
629..6996
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                                                                                                                                                         *tag=
                                                                                                                                                                                                                                                    0703
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are useful for synthesising simply atted oligosaccharides such as ganglioside, lysoganglioside or their mimics. Glycosyltransferases are useful for chemo-enzymatic synthesis of oligosaccharides, including gangliosides and other oligosaccharides that have including gangliosides and other oligosaccharides that have biological activity. The enzymes and nucleic acids that encode them are useful for studies of the pathogenesis mechanisms of organisms that synthesize ganglioside mimics, such as C. jejuni and the conclete acids are used as probes to study expression of genes involved in ganglioside mimetic synthesis. Antibodies raised against the glycosyltransferases are also useful for analyzing the expression patterns of these genes involved in pathogenesis. The oligonucleotides for inhibiting expression of the Campylobacter oligonucleotides for inhibiting expression of the Campylobacter carrymes that are involved in the biosynthesis of ganglioside mimics that can mask the pathogens from the host's immune system. The oligosaccharides are useful as diagnosing reagents or as therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A reaction mixture for the synthesis of a sialylated oligosaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and as immunogens for producing antibodies. Bacterial glycosyltransferase can be used to catalyse the formation of oligosaccharides that are identical to the corresponding mammalian structures and are asier and less expensive to produce in large quantity, compared to the mammalian glycosyltransferase. The bacterial origin of the enzymes facilitates expression of large quantities of the enzymes using relatively inexpensive prokaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAY97200, AAY97201, AAY97202, AAY97203, AAY97204, AAY97205
AAY97206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel glycosyltransferase polypeptides and polynucleotides useful biosynthesis of ganglioside and ganglioside mimics, as diagnostic reagents and as immunogen for producing antibodies
                                                                                                                                                                                                                                                                                                                                         /product = Lipooligosaccharide biosynthetic enzyme/note = "Open reading frame 12a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 11474 BP; 4506 A; 1495 C; 1613 G; 3860 T; 0 other;
                                                                                                                                                                                        /product= Sialic acid biosynthetic enzyme
                                                                                                                                                                                                                                                                   'product= CMP-sialic acid synthetase
                                 /product= CstII sialyltransferase
/note= "Open reading frame 7a"
6924..7964
                                                                                                                                                                                                                                                                                   /note= "Open reading frame 10a"
complement (10554..11366)
                                                                                                               'product = Sialic acid synthase
                                                                                                                                                                                                              "Open reading frame 9a"
                                                                                                                                  "Open reading frame 8a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 86-90; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CANA ) NAT RES COUNCIL CANADA.
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31-JAN-2000; 2000US-0495406.
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5048..6923
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9076..9
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                                                                                                                                    'note=
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for

DB 21; Length 11474;

2.7%; Score 79.2;

Query Match

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11364 GCCACAACTITCTAICATAATCCCGCTITITAATICITGCGATITIATCTCAAGAGCTIT 11305
                                                                                                                                                                                                 11244 TAAAGATAATAGTTTAAATATGGTTTTAGAATTTGCAAAAAAAGATCCAAGAATAAAAT 11185
                                                                                                                                                                                                                                                                                                                                                                                     11424 AAATTTCCTAAACTTTGATAGAATTGTTTTTATTTTTAACAAAATTTAGGAAAATAT 11365
                                                                                                                                                                          1416 AGATAGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGTTC 1475
                                                                                                                                                                                                                                         1476 AACAGATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCCTAGGGTACGCAT 1535
                                                                                                                                                                                                                                                                                                     CAT --- GICTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCCGTTTCTTTGC 1592
                                                                                                          1356 ACCITIAGITICIATITATATCCCCGCTTATAACTGTGCAAATTATATTCAAAGATGTGT 1415
                                             1296 AAAGGTACCTTACATCTATAGAAAGCTTTTACCAATAGAAGATTCACATATTCATAGAAT 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antinflammatory; cancer: eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                   TAAAGGTTATTACATTGGGCAGTTAGATTCAGATGATTATCTTGAGCCTGATGCAGTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTGTGTTTAAAAGAATTTTTAAAAGATAAAACGCTAGCTTGTGTTTATACC 1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 2331; 32pp + Sequence Listing; German
                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immune system associated gene SEQ ID NO: 2331.
Pred. No. 5.4e-06;
0; Mismatches 198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
   51.2%;
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                  211; Conservative
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Best Local Similarity
Matches 211; Conserv
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                invention provides a number of human immune system associated
                              genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
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                                                                                   macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilopsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6642
                                                                                                                                                                                                                                                                                                                6702
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                                                                                                                                                                                                                                                                             1992 AAAGAAAAACCATTTT$TTGTAGTCAATCAGTCATTAAATAGACAAGGCATCAATTATTA 2051
                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                  2052 TAATTATGACAAATTTGATGATTTAGATGAAAGTAGAAAGTATATCTTCAATAAAACCGC
                                                                                                                                                                                                                                                                                                                                                                                 2232 CAATATTATTGAATATAAAAATATATTCGTTATTATTCTACATGTTGATAAGAATCA
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                                                                                                                                                                                                     2.6%; Score 77.2; DB 24; Length 12237;
47.8%; Pred. No. 1.3e-05;
ve 0; Mismatches 278; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immune system associated gene SEQ ID NO: 1405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
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                                                                                                                                                                                                                                           Matches 255; Conservat
                                                                                                                                                                                                                         Similarity
                   present
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                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                            Local
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Homo sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                     Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2052 TAATTATGACAAATTTGATGATTTAGATGAAAGTAGAAAGTATATGTTCAATAAAACCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2112 TGAATATCAAGAAGAAATGGATATGTTAAAAGATCTTAAACTCCATTCAAAATAAAGATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAATCATGACAGCCTATTCGTTAAAAATGACAGCTATGCTTATATGAAAAATATGATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.6%; Score 77.2; DB 24; Length 17527; 43.9%; Pred. No. 1.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17527 BP; 4501 A; 296 C; 4094 G; 8636 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 1405; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 543;
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                                                                                                                                                                                                     Berlin
                                                                                                                30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
                                                                                02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 434; Conservative
                                                                                                                                                                                                     Piepenbrock C,
                                                                                                                                                                                                                                                                                       for diagnosis and tre
cytosine methylation
                                                                                                                                                                   (EPIG-) EPIGENOMICS
                                                                                                                                                                                                                                     WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
            WO200200928-A2
                                                03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2352
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16107 TATCCCTATTAAAAATCAAAACTATCTCTCATATTTCCTTCAAACATAACTATAAATTA 16048
                      16467 TACGACCAAACTAACCAAAATAACGAAATCCCGTCTCTACTAAAAAACACACAAAAAAA 16408
                                                                                                2832 PACATCGACCTGACTTATATGCCTTGGGAACGAAAATTACAATGGACAAATGAACAAAT 2891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        numan; cytostatic; anti-tumour; metabolism; metabolic disease; liver;
solid tumour; cancer; cytosine methylation; epigenetic; eye; kidney;
single nucleotide polymorphism detection; SNP; stool; urine; lung;
cerebral-spinal fluid; intestine; brain; heart; prostate; breast;
DUSP2; EPHX2; QDFR; SGSH; SHWT2; SLC7A2; SLC7A4; TYMS; ds.
2532 CGGCATGAATTTCTCAGCATTAACACATGATTGGATCGAGAAAATCAATGCGCATCCACC 2591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid, useful for diagnosis and therapy of metabolic disease, solid tumour and cancers, comprises segment of chemically modified genomic sequences of genes associated with metabolism - \,
                                                                                                                                                                                                                                                                                               TATTTGGTTCCAATTTGCACTTTTAATCTTAGAAAAGAAAACCGGCCATGTATTTAATAA
                                                                                                                                                               16347 TACTTAAACCCAAAAAATAAAATTACTATAAACCTAAAATCCTACCATTACACTCCAACC
                                                                                                                                                                                                                                                                                                                                                                                             2892 TCAAAGTGCAAAAAAAGGCGAAAATATCCCCGTTAACAAGTTCATTAATAATAACAAC
                                                                   ATTTAAAAAGCTGATTAAAACCTATTTTAATGACAATGACTTAAGAAGTATGAATGTGAA
                                                                                                                                AGGGGCATCACAAGGTATGTTATGAAGTATGCGCTACCGCATGAGCTTCTGACGATTAT
                                                                                                                                                                                                TAAAGAAGTCATCACATCCTGCCAATCAATTGATAGTGTGCCAGAATATAAACACTGAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS63332 standard; DNA; 17527 BP
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07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EPIG-) EPIGENOMICS AG
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The invention relates to a nucleic acid (I) comprising a sequence at associated with metabolism such as DUSP2 (NM_004418). EPHX2 (NM_001979), CDPR (NM_000320), SGSH (NM_001979) (NM_001940). SIGH (NM_001979), SGSH (NM_001979), SHWT2 (NM_001971), SIGH (NM_001730), SGSH (NM_001731) and TYMS (NM_001071), SIGH (NM_004173) and TYMS (NM_001071), SIGH (NM_004173), SIGH (NM_004173), SIGH (NM_001071), SIGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 77.2; DB 24
Pred. No. 1.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genes, and related primers of the invention.
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16407 TTAACGAAACATAATAACACACCTATAATCCCAACTACTAAAAAACTAAATAAAT 16348
2652 AGGGGCATCACAAGGTATGTTATGAAGTATGCGCTACCGCATGAGCTTCTGACGATTAT 2711
                                   2532 CGCCATGAATTTCTCAGCATTAACACATGATTGGATCGAGAAAATCAATGCGCATCCACC 2591
                                                                                   2592 ATTTAAAAAGCTGATTAAAACCTATTTAATGACAATGACTTAAGAAGTATGAATGTGAA 2651
                                                                                                                                                                                       2712 TAAAGAAGTCATCATCCTGCCAATCAATTGATAGTGTGCCAGAATATAACACTGAGGA 2771
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	US-09-437-277-4	US-09-437-277-2	US-08-597-236-1	US-08-746-682A-1	US-08-998-416-186	US-08-998-416-288	US-08-998-416-1137	US-08-961-527-71	US-08-559-896B-1	US-08-487-826B-13	US-08-961-527-86	US-08-961-083-199	US-08-998-416-595	US-09-056-075-1	US-08-961-083-197	US-08-232-463-14	US-09-453-702B-121	US-07-867-106-2	US-08-998-416-191	US-08-446-855A-1	US-09-150-741-1	US-08-998-416-534	US-09-426-290-1	US-08-998-416-683	US-08-998-416-786	5231168-1	US-08-920-812-11
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œ	Query Match	100.0	50.5	2.5	2.5	2.5	2.4	2.4	2.3	2.5	2.1	2.0	2.0	2.0	1.9	1.9	1.9	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.7	1.7	1.7	1.7
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827 - 827 - 827 - 827 - 827 - 828 - 828 - 828 - 828 - 828 - 886 -	NIV POL	ore 2979; ed. No. 0; Mismatches	CAA CAA	A – A	GAA -	TAA	TAC
220-8 20-11-8 20-11-8 20-11-8 20-11-8 20-11-8	ALIGNMENT OF THE UN /437,277 in ASCII	297 No. natc	SAAG	FATA 	3660	rard IIII	5 = 5
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8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	ALIGN 37277 ST277 ST277 GRAFTING GRAFTING aved in R	So Pr	ACG	¥=¥	ACC -	AAT 	ACA ACA
	ALIGNME Application US/09437277 444447 THE BOARD OF RECENTS OF THE INVENTION: POLYMER GRAFTING BY ELICATION NUMBER: US/09/437,27 LING DATE: 1999-11-10 SEQ ID NOS: 6 WordPerfect 8.0 (saved in ASC 979 Pasteurella multocida		AY I I	ATA 	GAA	3400	36CA
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800105456780010545	SULT 1 Sequence 4, Application US/0943727 Sequence 4, Application US/0943727 Patent NO. 644447 GEBERAL INFORMATION: APPLICANT: THE BOARD OF REGENTS TITLE OF INVENTION: POLYMER GRAF FILL REPERENCE: 5820.55.1 CURRENT APPLICATION NUMBER: US/09 CURRENT FILING DATE: 1999-11-10 NUMBER OF SEQ ID NOS: 6 SOFUMARE: WordPerfect 8.0 (saved LENGTH: 2979 LENGTH: 2979 LENGTH: 2979 LENGTH: 2979 LENGTH: DNA ORGANISM: Pasteurella multocida -09-437-277-4	Query Match Best Local Matches 297		9 9	12	181	241
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GCGCATCCACCATTAAAAAGCTGATTAAAACCTATTTAATGACATGACTTAAGAAGT CAAGTGAATATTTACTAAATAATGACATCTCATATTACACGAGTAATAGACTAATAAAA **ACTGAGGCACATTTAAGTAATATAATAAATTAAGTCAGTTAAATCTAAATTGTGAATAC** AATAAAGATGCCAAAATCGCAGTCAGTATTTTCTATCCCAATACATTAAACGGCTTAGTG ATTGAAAACGCCGTGGATTATGACATGTTCCTTAAACTCAGTGAAGTTGGAAATTTAAA ATTGAAAACGCCGTGGATTATGACATGTTCCTTAAACTCAGTGAAGTTGGAAATTTAAA GCCTCAGCATCAAATGCAGCCGTTTCTTTGCTAAAGGTTATTACATTGGGCAGTTAGAT TCAGATGATTATCTTGAGCCTGATGCAGTTGAACTGTGTTAAAAGAATTTTTAAAAGAT CATCTTAATAAAATCTGCTATAACCGCGTATTACATGGTGATAACACATCCATTAAGAAA CTCGGCATTCAAAAGAAAAACCATTTTGTTGTAGTCAATCAGTCATTAAATAGACAAGGC GCCTCAGCATCAAATGCAGCCGTTTCTTTTGCTAAAGGTTATTACATTGGGCAGTTAGAT g ΟŸ QQ Qy Db Qγ g óγ ΩD δy g Ω g δý g δ qq qq δy ρp ΟY Ωý Ωp qq Qγ ōλ Ωp Ω QΥ g Qγ q QY a Ω

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400 AAAGATTTTCCTAAAGATCTTGTTCTTGCCATTGCCAGATCATGTTAATGATTTTACA 459	640 AACTTACCATGGGCAAAAATACGAACAAAAACTTGACATAAAGGTATGTAAGACAA 699	820 CTTACAGAACTATTAGAAGACAATGATATTTTAATTGGACCTAGAAATATGTGGAT 879 1 1 1 1 1 1 1 1 1	1060 TTTGTTGCCGGTAATGTTGCATAAGAATGCGTAAATAAAGTGGTTGGT
GT 2640 QY TT 2700 Db TT 2700 QY AT 2760 QY AT 2760 QY AT 2820 Db III QB20 Db III 2820 Db	CA 2880 QY TT 2940 Db TT 2940 Db TT 2940 QY OY	40 A0	12; 1; Gaps 1; Db 1; Gaps 1; Oy CACTC 120 CACT
GCGCATCCACCATTTAAAAAGCTGATTAAAACCTATTTAATGACAATGACTTAAGAAGT ATGAATGTGAAAGGGCATCACAAGGTATGTTTATGAAGTATGCGCTACCGCATGAGGTT ATGAATGTGAAAGGGGCATCACAAGGTATGTTATGAAGTATGCGCTACCGCATGAGCTT ATGAATGTGAAAGGGGCATCACAAGGTATGTTTATGAAGTATGCGCTACCGCATGAGCTT CTGACGATTATTAAAGAAGTCATCACATCCTGCCAATGATGATGTGCCGCAATATT AACACTGAGGATTATTAAAGAAGTCATCACATCCTGCCAATCAAT	GTATTTATAAAACATCGACCCTGACTTATATGCCTTGGGAACGAAATTACAATGACA AATGAACAAATTCAAAGTGCAAAAAAGGCGAAAATATCCCCGTTAACAATGATTATT 	RESULT 2 Sequence 2, Application US/09437277 Sequence 2, Application US/09437277 Parent No. 6444447 Sequence 2, Application US/09437277 Parent No. 6444447 GENERAL INFORMATION: APPLICANT: THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA TILE OF INVENTION: POLYMER GRAFTING BY POLYSACCHARIDE SYNTHASES: FILE REFERENCE: 5820.551 CURRENT FILING DATE: 1999-11-10 NUMBER OF SEQ ID NOS: 6 SOFTWARE: WordPerfect 8.0 (saved in ASCII format) SEQ ID NO 2 SOFTWARE: LENGTH: 2112 LENGTH: 2112 TYPE: DNA SOGANLENA: Pasteurella multocida 16.69437-277-2	COTE 1503.2; DB 4; Length 21 red. No. 0; Mismatches 348; Indels 2 AAGCATATAACAGCAATGACTATGAATTAG

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TATTACATTGGGCAGTTAGATTCAGATGATTATCTTGAGCCTGATGCAGTTGAACTGTGT 1659
                                                                                                                                                              TTAAAAGAATTTTTAAAAGGATAAAACGCTAGCTTGTGTTTATACCACTAATAGAAACGTC 1719
                                                                                                                                                                            1840 ACGGATGGATTTAACGAAAATATTGAAAACGCCGTGGATTATGACATGTTCCTTAAACTC 1899
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Sequence 1, Application US/08597236

Batent No. 5733765

GENERAL INFORMATION:
APPLICANT: STINGELE, Franscesca
APPLICANT: STINGELE, Franscesca
APPLICANT: MOLLET, Beat
TITLE OF INVENTION: LACTIC BACTERIA PRODUCING
TITLE OF INVENTION: LACTIC BACTERIA PRODUCING
TITLE OF INVENTION: EXOPOLYSACCHARIDES
NUMBER OF SEQUENCES: 19
CORRESPONDENCES: 19
CORRESPONDENCES: 1155 Avenue of the Americans
STREET: 1155 Avenue of the Americans
CITT: New York
STATE: New York
COUNTRY: U.S.A.
21P: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER PARAMEN: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.30
CURPLICATION NUMBER: US/08/597,236
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2101 AAAGATATTTAA 2112
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NAME/KEY: misc_feature
LOCATION: 11302..1222
OTHER INFORMATION: (pps k) on nucleotides 10392-11339"
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LOCATION: 13732..14305
OTHER INFORMATION: /function= "CDS on the
OTHER INFORMATION: complementary strand"
OTHER INFORMATION: /product= "orfz"
CLASSIFICATION: 426
PRIOR APPLICATION NOMBER: BP 95201669.9
APPLICATION NUMBER: BP 95201669.9
FILING DATE: 20-JUN-1995.
ATTORNEY/AGENT INFORMATION:
NAME: Fanucci A., Allan
REGISTRATION NUMBER: 30256
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14602 base pairs
TYPE: nucleic acid such pairs
TYPE: nucleic acid pairs
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NAME/KEY: CDS
LOCATION: 7736..8212
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LOCATION: 8221..9192
OTHER INFORMATION: /product= "eps!"
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NAME/TEX: CDS
LOCATION: 10392.11339
OTHER INFORMATION: /product= "epsk"
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LOCATION: 1807..2535
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LOCATION: 6425..7540
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LOCATION: 2547..3239
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LOCATION: 352..1803
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                                                                                                                                                                                                          Query Match 2.5%; Score 74.6; DB 1; Length 14602; Best Local Similarity 50.7%; Pred. No. 1e-07; Matches 179; Conservative 0; Mismatches 174; Indels 0;
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ZIP: 1036

ZIP: 1036

COMPUTER READBLE FORM:

MEDIUW TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATIOS SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/746,682A

FILING DATE: 14-NOV-1996

CLASSIFICATION ATA:

APPLICATION NUMBER: 08/597,236

FILING DATE: 20-JUN-1995

APPLICATION NUMBER: EP 95201669.9

FILING DATE: 20-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Fanucci A., Allan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: STINGELE, Franscesca
APPLICANT: STINGELE, Franscesca
APPLICANT: MOLLET, Beat
TITLE OF INVENTION: EACTIC BACTERIA PRODUCING
TITLE OF INVENTION: EXOPOLYSACCHARIDES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americans
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08746682A
Patent No. 5786184
                     terminator
                                                                          promoter
274..302
                                                                                                                                                 340..345
                                     230..252
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                                                                        NAME/KEY:
LOCATION:
FEATURE:
                 NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                             ; NAME/KEY:
; LOCATION:
US-08-597-236-1
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FEATURE
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NAME/KEY: misc_feature
LOCATION: 11302..1222
OTHER INFORMATION: /product- "CDS (eps L) covering CDS
OTHER INFORMATION: (eps k) on nucleotides 10392-11339"
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LOCATION: 13732.14305
OTHER INFORMATION: /function= "CDS on the
OTHER INFORMATION: complementary strand"
OTHER INFORMATION: /product="orfz"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 10392..11339
OTHER INFORMATION: /product= "epsk"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 12233..13651
OTHER INFORMATION: /product- "epsm"
FEATURE:
                                                                                                                                                                                                                   OTHER INFORMATION: /product- "epsa"
FEATURE:
NAME/KEY: CDS
LOCATION: 1807..2535
OTHER INFORMATION: /product- "epsB"
FEATURE:
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LOCATION: 2547..3239
OTHER INFORMATION: /product= "epsc"
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LOCATION: 3249..3995
OTHER INFORMATION: /product= "epsD"
FEATURE:
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OTHER INFORMATION: /product- "epsE'
FEATURE:
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LOCATION: 4898..5854
OTHER INFORMATION: /product= "epsF"
FEATURE:
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LOCATION: 6425.7540
OTHER INFORMATION: /product= "epsg"
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LOCATION: 7736..8212
OTHER INFORMATION: /product- "epsH"
FEATURE:
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LOCATION: 8221..9192
OTHER INFORMATION: /product- "epsl'
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LOCATION: 9285..10364
OTHER INFORMATION: /product= "epsJ"
REGISTRATION NUMBER: 30256
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14602 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
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230..252
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LOCATION: 352..1803
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NAME/KEY:
LOCATION:
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LOCATION:
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Mon Jan 6 18:39:49 2003
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                                                                                                                                                                                                1403 TTCAAAGATG¶GTAGATAGTGCTCTTAATCAACTGTTGTCGATCTCGAGGTTTGTATTT 1462
                                                                                                                              1343 ATATICATAGAATACCITTAGITICIATITATATCCCCGCITATAACIGIGCAAATIAIA 1402
                                                                                               Gaps
                                                                                                                                                                                                                                                                 1463 GTAACGATGGTTCAACAGATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATC
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                                                             Length 14602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1643 AIGCAGIIGAACIGIGIIIAAAAGAAIITIIAAAAAGAIAAAACGCIAGCIIGI
                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                             Score 74.6; DB 1;
Pred. No. 1e-07;
0; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: No. 6239264artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUI
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
FILING APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 186, Application US/08998416 Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF.
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mohr, Christine
Wendland, Jurgen
Knechtle, Philipp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
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ATTORNEY/AGENT INFORMATION:
                                                                 2.5%;
                                                                                                    Conservative
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   RBS
340..345
                                                                    Query Match
Best Local Similarity
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APPLICANT:
APPLICANT:
APPLICANT:
; NAME/KEY:
; LOCATION:
US-08-746-682A-1
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APPLICANT:
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                                                                                                    Matches 179;
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2379 CACGAGTAATAGACTAATAAAAACTGAGGCACATTTAAGTAATATTAATAATTAAGTCA 2438
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                                                                                                                                                                                                                                            2019 ICAGTCATTAAATAGACAAGGCATCAATTATATAATTATGACAAATTTGATGATTTAGA 2078
                                                                                                                                                                                                                                                                                                                                                                                                                  2199 CAATACATTAAACGGCTTAGTGAAAAACTAAACAATATTATTGAATATAAAAAATAT 2258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2079 TGAAAGTAGAAATATGTTCAATAAAACCGCTGAATATCAAGAAAAATGGATATGTT 2138
                                                                                                                                                                                                                                                                                                                                                                            251 TATTITAATAACTAATTTAAAATTTGAACATAGACTAAATAGTATTCATATTAAATATTA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 AATAAGTATTAATAATCAAATAATTAATTAATTAATAATGATAATAATAGTTTAAATAA 72
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             311 TATATTAATTATTGATAATCTATTTAATAATTATTAAAGAAAATAATAATAATAA
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                                                                                                                                                                                   Length 615;
                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                   273;
                                                                                                                                                                                      2; DB 4;
4.8e-08;
                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                     Score 74.2;
Pred. No. 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Philippsen, Peter APPLICANT: Pohlmann, Rainer APPLICANT: Steiner, Sabine APPLICANT: Mohr, Christine APPLICANT: Wendland, Jurgen APPLICANT: Knechtle, Philipp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3054 Cornwallis Road CITY: Research Triangle Park
                                          SEQUENCE CHARACTERISTICS:
LENGTH: 615 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                      Query Match 2.5%;
Best Local Similarity 46.6%;
Matches 238; Conservative
: 919-541-8587
919-541-8689
                            INFORMATION FOR SEQ ID NO:
                                                                                                                                             ORGANISM: PAG1074RP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6239264
GENERAL INFORMATION:
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    TELEPHONE:
                                                                                                                                                              US-08-998-416-186
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2111 CTGAATATCAAGAAGAAATGGATATGTTAAAAGATCTTAAACTCATTCAAAATAAAGATG 2170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2231 ACAATATTATTGAATATAAAAAATATATTCGTTATTATTCTACATGTTGATAAGAATC 2290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2291 ATCTTACACCAGACATCAAAAAAAATATTGGCTTTCTATCATAAGCACCAAGTGAATA 2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2351 TTTTACTAAATAATGACATCTCATATTACACGAGTAATAGACTAATAAAAACTGAGGCAC 2410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2411 ATTTAAGTAATATTAATTAAGTCAGTTAAATCTAAATTGTGAATACATCATTTTTG 2470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2171 CCAAAATCGCAGTCAGTATTTTCTATCCCAATACATTAAACGGCTTAGTGAAAAAACTAA 2230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATTAAAGAAAATAATAATATCTAATAATATTTTAATAACTAATTTAAAATTTGAACATA 220
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Pred. No. 3.4e-07;
0; Mismatches 284; Indels
                                                                                                                              OFTWARTS STREEN: PC-DUS/MS-DUS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION TATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. TIMOCHY
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPRAK: 919-541-8889
                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 288: SEQUENCE CHARACTERISTICS: LENGTH: 837 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
2.4%;
Best Local Similarity 46.9%;
Matches 253; Conservative C
                                                                               Floppy disk
                                                           COMPUTER READABLE FORM:
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                                                                                 MEDIUM TYPE:
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US-08-998-416-288
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                       COUNTRY:
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1999 AACCATTTTGTTGTTGTAGTCAATCAGTCATTAAATAGACAAGGCATCAATTATATAATTAT 2058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2179 GCAGTCAGTATTTTCTATCCCAATACATTAAACGGCTTAGTGAAAAAACTAAACAATATT 2238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2119 CAAGAAGAAATGGATATGTTAAAAGATCTTAAACTCATTCAAAATAAAGATGCCAAAATC 2178
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                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
OPERATUG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATONNEY/AGENT INFORMATION:
NAME: MAGISS, J. Timothy
REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 70.2; DB 4;
Pred. No. 3.9e-07;
                                                                                                                                                                                                                                                                                                            SEE: No. 6239264artis Corporation
: 3054 Cornwallis Road
Research Triangle Park
No. 6239264th Carolina
Y: USA
                                                                         APPLICANT: Philippsen, Peter APPLICANT: Pohlmann, Rainer APPLICANT: Steiner, Sabine APPLICANT: Steiner, Sabine APPLICANT: Wohr, Christine APPLICANT: Wendland, Jurgen APPLICANT: Knechtle, Philipp APPLICANT: Rebischung, Corinne TITLE OF INVENTION: GENOMIC DNA SEQUENCETITLE OF INVENTION: AND USES THEREOF NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
Patent No. 6239264
GRMDAY ---- 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 1137:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.4%;
Best Local Similarity 47.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 636 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 251; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) ORGANISM: PAG1692RP
US-08-998-416-1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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MOLECULE TYPE: I
ORIGINAL SOURCE:
US-08-998-416-1137/c
                                                                                                                                                                                                                                                                                                                                                                                                                 27709
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COUNTRY:
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6261 AACATATAAAAATATTGAGATTGTTGTCGTTAATGATGGTTCTACGGATGCTTCAGGTGA 6320
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APPLICANT: Patrick E. Duffy
APPLICANT: Christian F. Ockenhouse
TITLE OF INVENTON: SEQUESTRIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: Macintosh 7.5 SOFTWARE: Microsoft Word CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/559,89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08559896B Patent No. 6310046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAWE: Moran, John
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION POR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1956 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: John Moran
STREET: USA MRMC - MCMR-JA
CITY: FORT DETRICK, FREDERICK
STATE: MARYLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 514
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US-08-559-896B-1
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Sequence 71, Application US/08961527

Patent No. 6420135

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
ATITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391

CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGTTCAACAGATAATACCTTAGA 1493
                                                                                                                                                                                                                                                                        AATATTAATAAATTAAGTCAGTTAAATCTAAATTGTGAATACATCATTTTTGATAATCAT 2478
                                                                                                                                                                                      2418
         2239 ATTGAATATAAAAAATATATATTCGTTATTGTTGTTGATAAGAATCATCTTACA 2298
                                                  331 AATAAACAATTAATAAAAAATATATTAATTGATAATCTATTTAATAATTTAAAG 272
                                                                                                                                        271 AAAATAATAATAATATATAATATTTTAATAACTAATTTAAAATTTGAACATAGACTAAAT 212
                                                                                                                                                                                                                    2299 CCAGACATCAAAAAAGAAATATTGGCTTTCTATCATAAGCACCAAGTGAATATTTACTA
                                                                                                                                                                                      AATAATGACATCTCATATTACACGAGTAATAGACTAATAAAAACTGAGGCACATTTAAGT
                                                                                                                                                                                                                                                                                                                   2.3%; Score 67.2; DB 4; Length 32768; ilarity 44.9%; Pred. No. 6e-06; Conservative 0; Mismatches 313; Indels 0;
                                                                                                                                                                                                                                                                                                                                                               2479 GACAGCCTATTCGTTAAAATGACAGCTATGCTTATATGAAAAAATATGAT 2529
                                                                                                                                                                                                                                                                                                                                                                                                      GATAATAATAGTTTAAATTTTAATACTTAAATATTATAATAAAAAAGTT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Brookes, A. Anders
REGISTATION UNDBER: 36,331
REFERENCE/DOCKET NUMBER: PB34(
TELECOMMUNICATION INFORMATION:
TELEPAX: (301) 309-8514
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 32768 base pairs
nucleic acid
EDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20850
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US-08-961-527-71
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Matches 25
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1854 CGAAAATATTGAAAACGCCGTGGATTATGACATGTTCCTTAAACTCAGTGAAGTTGGAAA 1913 1734 CITAATCGCIAATGGTTACAATTGGCCAGAATTTTCACGAGAAAACTCACAACGGCTAT 1793 1554 CGGAATAGCCTCAGCATCAAATGCAGCCGTTTCTTTTGCTAAAGGTTATTACATTGGGCA 1613 1674 AAAAGATAAAACGCTAGCTTGTGTTTATACCACTAATAGAAACGTCAATCCGGATGGTAG 1733 AGAGTATCAGGCTGATATTGCAGTTGGTAATTATTATTCTTTCAACGAAAGTGAAGGAAT 6560 1494 AGTGATCAATAAGCTTTATGGTAATAATCCTAGGGTACGCATCATGTCTAAAACCAAATGG 6321 AATTTGTAAAGAATTTTCAGAAATGGATCACCGAATTCTCTATATAGAACAAGAAAATGC 6621 CTTTGAGAACTTGTATGAAACTCAAGAAATGAAGAGTTTTGCTTTGATATCTGCTTGGGG 6681 IAAACICIAIAAGGCAAGATIGITIGAGCAGTIGCGCTITGACATAGGTAAATTAGGAGA 1614 GITAGAITCAGAIGAITAICITGAGCCTGAIGCAGITGAACTGIGITIAAAAGAAITITI 6561 GTTCTACTTTCATATATTGGGAGACTCCTATTATGAGAAAGTATATGATAATGTTTCTAT 6381 TGGTCTTTCTGCCGCACGAAACACCGGTCTGAATAATATGTCCGGAAATTATGTGACCTT

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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDN
                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ANTI-SENSE: NO US-08-487-826B-13
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                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
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US-08-961-527-86/c
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APPLICANT: SIM, Kim L.
APPLICANT: SIM, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Milet. Louis
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas
APPLICANT: Wellems, Thomas
APPLICANT: APPLICANT: AND PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEDIENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSE: Knobbe Martens Olson & Bear
                                                                                                                                          ä
                                                                                                                                                                               1987 ATTCAAAAGAAAACCATTTTGTTGTAGTCAATCAGTCATTAAATAGACAAGGCATCAAT 2046
                                                                                                                                                                                                                                                          2047 TATTATAATTATGACAAATTTGATGATTTAGATGAAAGTAGAAAGTATATCTTCAATAAA 2106
                                                                                                                                                                                                                                                                                                                                                               1348 CGAAATTTAGACAAGGATAAAGGAGCCAAGATAGAAGATATTATAGACTATTTTAACAAA 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2287 AATCATCTTACACCAGACATCAAAAAAGAAATATTGGCTTTCTATCATAAGCACCAAGTG 2346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2347 AATATTTTACTAAATAATGACATCTCATATTACACGAGTAATAGACTAATAAAAACTGAG 2406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCACATITAAGTAATATAAATTAAGTCAGTTAAATCTAAATTGTGAATACATCATT 2466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2467 TTTGATAATCATGACAGCCTATTCGTTAAAAATGACAGCTATGCTTATATGAAAAAATAT 2526
                                                                                                                                                                                                                                                                                               1288 TTAAATAATAAGCACACAAATAATAATTAATGAAAATGTAGAAGTTGAATTAGTTGTA 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAATTAAAAAAGACAAAAATGTTAATGTTTCCAATATAGTGAATTTTTTAAATTCAAAA 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAAATATTCAGATTATTCAAGAGGATAATATAAAAAATAAAGGCCAAAAGGATAACACT 1587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1702 AACAATGTTGATGGTATAAAAATGTTGATGGTATAAAAATGTTGATGGTATAAAAAT 1761
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1762 GTTGATGGTATAAACAATGTGGGAGATATAAACAATGCTGGAGATACAAATAATGC 1817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATGTCGGCATGAATTTCTCAGCATTAACACATGATTGGATCGAGAAAATCAATGC 2582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2227 CTAAACAATATTATTGAATATAAAAAATATATTCGTTATTATTCTACATGTTGATAAG
                                                                                                                                                                                                                                                                                                                                        ACCGCTGAATATCAAGAAGAAATGGATATGTTAAAAGATCTTAAACTCATTCAAAATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                     GATGCCAAAATCGCAGTCAGTATTTCTATCCCAATACATTAAACGGCTTAGTGAAAAAA
                                                                                                                                          9
                                                                                                 Score 66.8; DB 4; Length 1956;
Pred. No. 3.2e-06;
0; Mismatches 317; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/08487826B Patent No. 5993827
                                                                                                   Query Match 2.2%;
Best Local Similarity 45.8%;
Matches 273; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
TYPE: Nucleic acid
STRANDEDNESS: Double
                                           Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                  STRANDEDNESS:
; TOPOLOGY: Line
US-08-559-8968-1
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Streptococcus pneumoniae Polynucleotides and Sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1972 ATTAAGAAACTCGGCATTCAAAAGAAAAACCATTTTGTTGTTGTAGTCAATCAGTCATTAAAT 2031
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SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/487,826B FILING DATE: 10-SEP-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 86, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptcoccus
                                                                                                                CLASSIFICATION: 43.2
ATTORNEY, AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
RREFRERENCE/POCKET NUMBER: NIH1:
TELEPHONE: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.1%;
Best Local Similarity 47.5%;
Matches 250; Conservative
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APPLICANT: Choi et. al.
TITLE OF INVORTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 19390;
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0; Mismatches 175; Indels
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                                                                                                                    ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
                               ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 61;
Pred. No. 0
                                                                                                                                                                                         OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII TEAX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
                                                                                                                                                                                                                                                                                                                                                                     NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-961-083-199
; Sequence 199, Application US/08961083
; Patent No. 6159469
                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.0%;
Best Local Similarity 48.7%;
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 19390 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NUMBER OF SEQUENCES: 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   double
                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                  CORRESPONDENCE ADDRESS:
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                                                                                     Maryland
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                                                                                                     COUNTRY:
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US-08-961-527-8
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.651 GAACIGIGITITAAAAGAATITITAAAAGATAAAACGCTAGCTIGIGITITATACCACTAAI 1710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .771 CGAGAAAAACTCACAACGGCTATGATTGCTCACCATTTTAGAATGTTTACGATTAGAGCT
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
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Pred. No. 8.1e-05;
0; Mismatches 294;
Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                        FILLING DAALE:
ATTORNEY/GENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36.33
REFERENCE/DOCKET NUMBER: PB340P2
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
LENGTH: 2023 base pairs
                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
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Best Local Similarity 44.69
Matches 237; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
  E: Human
9410 Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                        STREET: 9410 Key CITY: Rockville
                                                                    STATE: Maryland COUNTRY: USA
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US-08-961-083-199
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2341 CAAGTGAATATTTTACTAAATAATGACATCTCATATTACACGAGTAATAGACTAATAAAA 2400
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NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                            RESULT 14
US-09-056-075-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: W
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    547 AATAAAATAGAAATAGAAATAGCATATATTATGTTCACAAAATACAATCTATATAG 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Best Local Similarity 48.0%; Pred. No. 0.00015;
Matches 168; Conservative 0; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSE: No. 6239264artis Corporation
STREET: 3054 COrnwallis Road
CITY: Research Triangle Park
CATRE: 0539264th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US./08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION ATA:
APPLICATION NATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATONNEY AGENT INFORMATION:
NAME: Melgs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306,
TELEPHONE: 919-541-8587
                                 US-08-998-416-595/c
: Sequence 555, Application US/08998416
: Patent No. 6239264
: GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
Mohr, Christine
Wendland, Jurgen
Knechtle, Philipp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 595:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 658 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-998-416-595
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APPLICANT:
APPLICANT:
APPLICANT:
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1852 AACGAAAATATTGAAAACGCCGTGGATTATGACATGTTCCTTAAACTCAGTGAAGTTGGA 1911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3337 TATTTGATAAAACATATTTAAAGATATTAATCAAATCCTGTAAAGATGAAAATGAAAATAA 3278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1972 ATTAAGAAACTCGGCATTCAAAAGAAAACCATTTTGTTGTAGTCAATCAGTCATTAAAT 2031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: 3770..4013
OTHER INFORMATION: /note= "RP4 origin of DNA transfer (oriT) from
OTHER INFORMATION: plasmid RP4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 6243
                                                      2401 ACTGAGGCACATTTAAGTAATATTAATAAATTAAGTCAGTTAAATCTAAA 2450
                                                                                 Sequence 1, Application US/09056075

Patent No. 595368

GENERAL INFORMATION:
APPLICANT: Johnson, Eric A.
APPLICANT: Broad, Julian:
TITLE OF INVENTION: Expression System for Clostridium:
TITLE OF INVENTION: Species
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 362; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/056,075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.9%; Score 57.8; DB 2; 45.0%; Pred. No. 0.00048;
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us-09-842-484a-1.rni

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2152 CICATICAAAATAAAGAIGCCAAAAICGCAGICAGIATITICIAICCCAAIAAAAC 2211
                                                                                                                                                                                              3102 AATATTACAAAAAGTATTGTTAAAATTGAAAAATTAAATCTTTAGTATCTTTGGAAATA 3043
                                                                                                                                                                                                                                      2212 GGCTTAGTGAAAAAACTAAACAATATTATTGAATATAAAAAAATATATTCGTTATTATT 2271
                                                                                                                                                                                                                                                               2332 CATAAGCACCAAGTGAATATTTACTAAATAATGACATCTCATATTACACGAGTAATAGA 2391
                                                                                                                                                                                                                                                                                                                                                                                                                             2392 CTAATAAAAACTGAGGCACATTTAAGTAATATTAATAATTAAGTCAGTTAAATCTAAAT 2451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2862 GITTAAAATATITTAATAAAAATAATAAATTAAAACATAAAAATAGATTAAGTTTCAAT 2803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 197, Application US/08961083
Sequence 197, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2452 TGTGAATACATCATTTTTGATAATCATGACAGCCTATTCGTTAAAAATGACAGCTATGCT
                                                                             2092 TATATCTTCAATAAAACCGCTGAATATCAAGAAGAAATGGATATGTTAAAAGATCTTAAA
                                                                                                                                                                                                                                                                                                                                                              2982 TAAAAACTAAAATTAGTAAATCATCTAAATATTACAAATGAAGAAATATTATTTGTAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: MATYland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Brookes, A. Anders
REGISTRATION INDRER: 36,373
REFERENCE/DOCKET NUMBER: PB34(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ. ID NO: 197:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                           1531 CGCATCATGTCTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCCGTTTCTTT 1590
                                                                                                                                                                                                                                                                                                                                                          1591 GCTAAAGGTTATTACATTGGGCAGTTAGATTCAGATGATTATCTTGAGCCTGATGCAGTT 1650
                                                                                                                                                                                                                                                  2 TGTTTGGATAGCATTCAGAATCAGACGTATCAAAATTTTGAGTGTTTATTAATCAATGAT
                                                                                                                                ;
0
                                                                                             Length 811;
                                                                                                                                Indels
                                                                                             Score 57.6; DB 3;
Pred. No. 0.00029;
0; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                            1651 GAACTGTTTAAAAGAATTTTTAAAAGATAA 1682
                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 GACCGATTATATGGTGCTTTGAAAAAGGAAAA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            completed: January 4, 2003, 00:40:18
ne : 314 secs
                                                                                                    1.9%;
LENGTH: 811 base pairs
TYPE: nucleic acid
STRANBEDNESS: double
JOPOLOGY: linear
US-08-961-083-197
                                                                                                    Query Match
Best Local Similarity 50.7%
Matches 138; Conservative
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January 3, 2003, 23:56:15 ; Search time 168 Seconds (without alignments) 7669.230 Million cell updates/sec
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                     381593 seqs, 216252194 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                               - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                      US-09-842-484A-1
2979
                                                                                                                                                                                                        Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

1: /cggn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cggn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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14: /cgn2_6/ptodata/1/pubpna/US00_PUBCOMB.seq:*

Published_Applications_NA:*

Database

SUMMARIES

	Description	Sequence 9, Appli	Sequence 137, App	Sequence 3, Appli	Sequence 1, Appl1	Sequence 83, Appl	Sequence 9, Appli	Sequence 29, Appl	٠,	Sequence 28, Appl		Sequence 26, Appl	m	Sequence 199, App	Sequence 5785, Ap	Sequence 5558, Ap	, ,	1, 2		Sequence 4, Appli
	QI	US-09-879-959-9	US-09-070-927A-137	US-09-900-038A-3	US-09-816-028A-1	US-09-870-759-83	US-09-767-041-9	US-09-767-041-29	US-09-816-028A-30	US-09-816-028A-28	US-09-351-794A-1	US-09-816-028A-26	US-09-070-927A-308	US-09-765-272-199	US-09-960-352-5785	US-09-960-352-5558	US-09-765-272-197	US-09-790-988-1	US-09-960-352-3400	US-10-051-952-4
	09	6	10	10	10	6	10	10	10	10	10	10	10	10	10	10	10	10	10	12
	Query Match Length DB	2937	5550	6865	11474	17276	6992	6992	891	912	1956	906	2406	2023	516	431	811	640681	446	3876
æ	Query	76.6	2.9	2.7	2.7	2.5	2.5	2.5	2.3	2.3	2.2	2.5	2.1	2.0	7.0	2.0	1.9	1.9	1.8	1.8
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Sequence 4292, Ap Sequence 2109, Ap Sequence 12872, A Sequence 673, App Sequence 673, App Sequence 5301, Ap Sequence 5301, Ap Sequence 1221, Ap Sequence 1221, Ap Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 201, App Sequence 3, Appl Sequence 201, App Sequence 201, App Sequence 3, Appl Sequence 520, Appl Sequence 54, Appl Sequence 51, App
US-09-878-574-4292 US-09-9813-965-2109 US-09-960-352-573 US-09-801-641-40 US-09-960-352-5583 US-09-960-352-5583 US-09-960-352-5831 US-09-960-352-5831 US-09-960-352-5831 US-09-960-352-12211 US-09-960-352-12211 US-09-960-352-12211 US-09-918-842A-4090 US-09-960-352-4582 US-09-960-352-4582 US-09-960-352-4583 US-09-960-352-4584 US-09-960-352-4584 US-09-960-352-4584 US-09-960-352-4584 US-09-960-352-4584 US-09-960-352-4584 US-09-960-352-4584 US-09-960-352-4584 US-09-960-352-4584 US-09-960-352-5087
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ALIGNMENTS

S - S - S - S - S - S - S - S - S - S -	-9 US20020160489A1 US20020160489A1 ORMATION: Weigel, Paul H Weigel, Rshama Denngelis, Paul NVENTION: IN BACILLUS SUBTILIS ENCE: 3554.049 ELICATION NUMBER: US/09/879,959 LICATION NUMBER: 09/469,200 NG DATE: 1999-12-21 ICATION NUMBER: 09/178,851 NG DATE: 1999-12-21 ICATION NUMBER: 09/178,851 NG DATE: 1999-10-26 SEQ ID NOS: 10 Patentin version 3.1 pasteurella multocida
υш	 Score 2283.4; DB 9; Length 2937; Pred. No. 0;
- 4	_
Qy Db	43 ATTTTAAAGGAAAGAAATGAATACATTATCACAAGCAATAAAAGCATATAACAGCAAT 102
OY Db	103 GACTATGAATTAGCACTCAAATTATTGAGAAGTCTGCTGAAACCTACGGGCGAAAATC 162
δ	163 GTTGAATTCCAAATGTAAAGAAAAACTCTCGACCAATTC 209
Qy	210TTATGTAAGTGAAGATAAAAAAAGGGGTTGCGATAGCTCATTAGATATC 261

2100 2220 2301 2361 2400 2061 2121 2181 2001 1461 AATGACATCTCATATTACACGAGTAATAGACTAATAAAAACTGAGGCACATTTAAGTAAT AACCGCGTATTACATGGTGATAACACATCCATTAAGAAACTCGGCATTCAAAAGAAAAAC GAAGAAATGGATATGTTAAAAGATCTTAAAACTCATTCAAAATAAAGATGCCAAAAATCGCA GAATTTTCACGAGAAAACTCACAACGGCTATGATTGCTCACCATTTTAGAATGTTTACG ATTAGAGCTTGGCATTTAACGGATGGATTTAACGAAAATTTGAAAACGCCGTGGATTAT GACATGTTCCTTAAACTCAGTGAAGTTGGAAAATTTAAAACATCTTAATAAAATCTGCTAT CATITIGITGIAGICAATCAGICATIAAATAGACAAGGCAICAATIAITATAATAIGAC **AAATTTGATGATTTAGATGAAAGTAGAAAGTATATCTTCAATAAAACCGCTGAATATCAA** GATATTATGAGAGAAAAGGTCCCTTATATCTATAGAAAACTTTTACCAATAGAAGATTCG ATTCAAAGATGTGTAGATAGTGCTCTTAATCAAACTGTTGTGTGGACTGCGAGGTTTGTATT **ACCACTAATAGAAACGTCAATCCGGATGGTAGCTTAATCGCTAATGGTTACAATTGGCCA** TGTAACGATGGTTCAACAGATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAAT CCTAGGGTACGCATCATGTCTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCC GTTTCTTTTGCTAAAGGTTATTACATTGGGCAGTTAGATTCAGATGATTATCTTGAGCCT 2362 1822 1882 1861 1942 1921 2002 1981 2062 2041 2122 2182 2242 2221 2302 2281 1702 1681 1762 1741 1801 2101 2161 1441 1582 1561 1261 1342 1321 1402 1381 1462 1522 1501 Dβ 셤 a QΥ qq ŏ g Db qq Qγ QΥ δy QΥ δ g q δ Dp ŏ g QΥ d Qγ Dp δŽ Op Qγ Dβ δ qq g δy Ω δ Qγ

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APPLICANT: Miyake, Katsuhide
APPLICANT: Matanabe, Masaki
APPLICANT: Matanabe, Masaki
APPLICANT: Ijima, Shinji
TITLE OF INVENTION: Beta 1,3-galactosyltransferase and DNA encoding the same
FILE REFERENCE: 766.53
CURRENT APPLICATION UNMBER: US/09/900,038A
CURRENT APPLICATION NUMBER: US 2001-09-21
PRIOR APPLICATION NUMBER: JP 2001-392
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1414 GTAGATAGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGT 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1534 ATCATGTCTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCGGTTTCTTTTGCT 1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTATCCATAAAGAAAATGGTGGGCTAAGCGATGCTCGTAATGCTGGAATTGAAATAGCA 1240
                                                                                                                                                                                                                                                                                                                                                                                                                  1001 ATGCCCAAAATTAGTATTATTGTTCTGTATACAATGTAGAAAAATATTAGAAAAATGT 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAACAGATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCCTAGGGTACGC 1533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1594 AAAGGTTATTACATTGGGCAGTTAGATTCAGATGATTATCTTGAGCCTGATGCAGTTGAA 1653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1354 ATACCTTTAGTTTCTATTTATATCCCCGCTTATAACTGTGCAAATTATATTCAAAGATGT 1413
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                               Length 5550;
                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                 2.9%; Score 86; DB 10; L
54.0%; Pred. No. 6.8e-08;
tive 0; Mismatches 150;
                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 137:
  REFERENCE/DOCKET NUMBER: PB369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Streptococcus agalactiae type FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-6804
TELEFAX: (301) 309-6812
INFORMATION FOR SEQ ID NO: 137:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 3, Application US/09900038A
; Patent No. US20020142425A1
; GENERAL INFORMATION:
                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 5550 base pairs
                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                       Best Local Similarity 54.0°
Matches 176; Conservative
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CDS
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LOCATION:
NAME/KEY: C
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LENGTH: 68
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
                                                                                                                                                                                                                                                                               TICTCAGCATTAACACATGATTGGATCGAGAAAATCAATGCGCATCCACCATTAAAAAG 2601
                                                                                                                                                                                                                                                                                                                                                                    2641 CAAGGTATGTTTATGACGTATGCGCTAGCGCATGAGCGTTCTGACGATTATAAAGAAGTC 2700
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                                                                                                                                                                                                                  2521 TTCTCAGCATTAACACATGATTGGATCGAGAAAATCAATGCGCATCCACCATTTAAAAAG 2580
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  ATTAATAAATTAAGTCAGTTAAATCTAAATTGTGAATACATCATTTTTGATAATCATGAC
                                                                                   AGCCTATTCGTTAAAAATGACAGCTATGCTTATATGAAAAAATATGATGTCGGCATGAAT
                                                                                                                                                                                                                                                                                                                                                2662 CAAGGTATGTTATGAAGTATGCGCTACCGCATGAGCTTCTGACGATTATAAAGAAGTC
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM, MSDOS Version 6.2
SOFTWARE: ASCII Fext
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/070,927A FILING DATE: 04-May-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. HOOVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 137, Application US/09070927A Patent No. US20020120116A1 GENERAL INFORMATION:
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Patrick J. Dillon
Steven Barash
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NAME/KEY: CDS
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US-09-870-759-83
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Sequence 1, Application US/09816028A

Patent No. US20020042369A1

SEMERAL INFORMATION:

APPLICANT: Gilbert, Michel

APPLICANT: Makarchuk, Warren W.

APPLICANT: National Research Council of Canada

TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of

TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of

TITLE OF INVENTION: Gangliosides and Ganglioside Mimics

CURRENT APPLICATION NUMBER: US/09/816,028A

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: US 60/118,213

PRIOR APPLICATION NUMBER: US 60/118,213

PRIOR APPLICATION NUMBER: US 60/118,213

PRIOR PRILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 49

SEGTWARER PREED PATENTING DATE: 2000-01-31

SEGTWARER PREED PATENTING DATE: 2000-01-31
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                                                                                                                                                          1361 TAGTTTCTATTTATATCCCCGCTTATAACTGTGCAAATTATATTCAAAGATGTGTAGATA 1420
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                                                                                    Length 6865;
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Best Local Similarity 51.2%; Pred. No. 1.7e-06;
Matches 211; Conservative 0; Mismatches 198;
                                                                                    DB 10;
                                                                                  Score 80.6; DB 10;
Pred. No. 8.1e-07;
0; Mismatches 149;
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ORGANISM: Campylobacter jejuni
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                                                                                      2.7%;
                                                                                                                       Conservative
(3982)..(4953)
CDS
                         ; LOCATION: (5009)..(5947)
US-09-900-038A-3
                                                                                                       Best Local Similarity
Matches 170; Conserva
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US-09-816-028A-1/c
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 LOCATION:
NAME/KEY:
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                                                                                      Query Match
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APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
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                                                              11304 GCAAAGTTGTATAAATCAGACTTTAAAAGATATTGAAATTTTGATTATCGATGATAAAAG 11245
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1416 AGATAGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGTTC 1475
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                                                                                                                            AACAGATAATAACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCCTAGGGTACGCAT
                                                                                                                                                                                                                                                     CAT -- - GTCTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCCGTTTCTTTTGC
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Pred. No. 1.8e-05;
0; Mismatches 213;
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CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: Patentin version 3.1
SEQ ID NO 83
LENGTH: 17276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 83, Application US/09870759 Patent No. US20020177551A1
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Best Local Similarity 48.7%;
Matches 202; Conservative
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US-09-870-759-83
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us-09-842-484a-1.rnpb

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INVENTION:
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                                                                                                                                                                                                              SEQ ID NO 29
                                                                                                                                                                                                                                                   TYPE: DNA
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                                                                                                                                Sequence 9, Application US/09767041

Fatent No. US20020055168A1

GENERAL INFORMATION:
STREPTOCOCCUS SUIS VACCINES AND DIAGNOSTIC TESTS
FILE REPRENCE: 2183-4726

CURRENT APPLICATION NUMBER: US/09/767,041

CURRENT FILING DATE: 2001-01-22

PRIOR PILICATION NUMBER: EP98202465.5

PRIOR FILING DATE: 1999-07-19

PRIOR FILING DATE: 1998-07-22

PRIOR FILING DATE: 1998-07-22

PRIOR FILING DATE: 1998-07-22

PRIOR FILING DATE: 1998-07-22

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PATENTING DATE: 1998-07-22

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PATENTING DATE: 1998-07-22

LENGTH: 6992
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           1632 TCTTGAGCCTGATGCAGTTGAACTGTTTTAAAAGAATTTTTAAAAGATAAAACG 1686
                                   9502 AGTTTCCTCTGATTACATAGCGAATTTGTATAATGCTATTCAAAAACATGATTCG 9556
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Pred. No. 2.2e-05;
0; Mismatches 203;
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APPLICANT: Smith, Hilda
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Best Local Similarity 49.0%;
Matches 195; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Streptococcus suis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: misc_feature
; LCCATION: (1)..(6992)
; OTHER INFORMATION: CPS 2
US-09-767-041-9
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US-09-767-041-9
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Sequence 30, Application US/09816028A

Fatent No. US20020042369A1

GENERAL INFORMATION:
APPLICANT: Gilbert, Michel
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wational Research Council of Canada
TITLE OF INVENTION: CamplyLobacter Glycosyltransferases for Blosynthesis of
TITLE OF INVENTION: Camplosides and Ganglioside Mimics
TITLE OF INVENTION: Canadiosides and Ganglioside Mimics
CURRENT PILING DATE: 2001-03-21
FRIOR PELICATION NUMBER: US 60/118,213
FRIOR PELICATION NUMBER: US 60/118,213
FRIOR PELICATION NUMBER: US 09/495,406
FRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 49

SOFTWARE: Patentin Ver. 2.1
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STREPTOCOCCUS SUIS VACCINES AND DIAGNOSTIC TESTS
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                    FILE REFERENCE: 2183-4726
CURRENT APPLICATION NUMBER: US/09/767,041
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: EP98202465.5
PRIOR FILING DATE: 1999-07-19
PRIOR FILING DATE: 1998-07-29
PRIOR FILING DATE: 1998-07-22
PRIOR PAPLICATION NUMBER: EP98202465.5
PRIOR PAPLICATION NUMBER: EP98202467.1
PRIOR APPLICATION NUMBER: EP98202467.1
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.0
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Pred. No. 2.
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Best Local Similarity 49.0°
Matches 195; Conservative
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CTHER INFORMATION: CPS1
US-09-767-041-29
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US-09-351-794A-1
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APPLICANT: Gilbert, Michel
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wakarchuk, Warren W.
APPLICANT: National Research Council of Canada
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Campylobacter Gilycosyltransferases for Biosynthesis of
TITLE OF INVENTION: Campylobacter Gilycosyltransferases for Biosynthesis of
TITLE OF INVENTION: Cangliosides and Ganglioside Mimics
FILLE REFERENCE: 019633-0001110S
FILLE REFERENCE: 019633-000110S
FILLE REPRENCE: 2001-03-21
FRIOR PRICATION NUMBER: US 60/118,213
FRIOR FILLING DATE: 1999-02-01
FRIOR PRICATION NUMBER: US 09/495,406
FRIOR FILLING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 28
LENGTH: 912
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COTHER INFORMATION: Campylobacter glycosyltransferase B (CgtB) beta-1,3

OTHER INFORMATION: galactosyltransferase from C. jejuni serotype 0:2

COTHER INFORMATION: (strain NCTC 11168)

US-09-816-028A-28
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                                                                                                    COTHER INFORMATION: beta-1,3 galactosyl transferase from C. jejuni 0:10 US-09-816-028A-30
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ilarity 53.2%; Pred. No. 0.0002;
Conservative 0; Mismatches 143;
                                                                                                                                                                      Score 68.4; DB 10;
Pred. No. 0.00011;
0; Mismatches 151;
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                                   TYPE: DNA
ORGANISM: Campylobacter jejuni
                                                                                                                                                                          Query Match 2.3%;
Best Local Similarity 52.8%;
Matches 172; Conservative
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Matches 166;
                                                                                      NAME/KEY: CDS
SEQ ID NO 30
LENGTH: 891
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                                                                                                                                                                                                                                                                                                                                                                              1599 TIATTACATTGGGCAGTTAGATTCAGATGATTATCTTGAGCCTGATGCAGTTGAACTGTG 1658
1362 AGTITCTATITATATCCCGCTTATAACTGTGCAAATTATATTCAAAGATGTGTAGAFG 1421
                                                                                                                                                                                                                                     249 ACCTTATATCTTTTTAGATTCTGATGATTATTTAGAACTTAATGCTTGCGAAGAATG 308
                                            9 AATITICCATCATACTACCAACTTATAATGTGGAAAAATATATTGCTAGAGCATTAGAAAG
                                                                                                                       69 TIGCATTAACCAAACTTTTAAAGATATAGAAATCATTGTAGTAGATGATGTGAATGA
                                                                                                                                                                                                                                                                                                                                189 TAATGAAGAGATTTAAAGCTTTTAAGAGCAAGATATGAAGGTGCTAAAGTAGCAACTTC
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45.8%; Pred. No. 0.00028;
tive 0; Mismatches 317;
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Query Match
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Fatent No. US20020042369A1

GENERAL INFORMATION:
APPLICANT: Gilbert, Michel
APPLICANT: Watron W.
APPLICANT: Wational Research Council of Canada

TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
TITLE OF INVENTION: Ganqliosides and Ganglioside Mimics

FILE REFERENCE: 019633-0001110S

CURRENT APPLICATION NUMBER: US/09/816,028A

CURRENT FILING DATE: 2001-03-21

FRIOR FILING DATE: 1999-02-01

FRIOR FILING DATE: 2000-01-31

FRIOR FILING DATE: 2000-01-31

FRIOR FILING DATE: 2000-01-31
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OTHER INFORMATION: beta-1,3-galactosyltransferase from C. jejuni strain
OTHER INFORMATION: OH4384 (ORF 6a of lipooligosaccharide (LOS)
OTHER INFORMATION: biosynthesis locus)
                                          AATATTTTACTAAATAATGACATCTCATATTACACGAGTAATAGACTAATAAAAACTGAG 2406
                                                                                                                           2407 GCACATITIAAGTAATATTAAATTAAGTCAGTTAAATCTAAATTGTGAATACATCATT 2466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1422 TGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGTTCAACAGA 1481
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1528 AAAAATATTCAGATTATTCAAGAGGATAATATAAAAAATAAAGGCCAAAAGGATAACACT 1587
                                                                                  1588 GAAATGTTAGATAATAATGAAAGGAAATA----ACAAATATTGATATAAAAATGTTGAT 1641
                                                                                                                                                                     2467 TITGATAATCATGACAGCCTATTCGTTAAAAATGACAGCTATGCTTATATGAAAAAATAT 2526
                                                                                                                                                                                                                                                          1702 AACAATGTTGATGGTATAAAAATGTTGATGGTATAAAAAATGTTGATGGTATAAAAAT 1761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 CAATGAAAAAACTTAGGTCTTTTAAGAGCAAGATATGAAGGTGTGAAAGTAGCAAACTC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 TCCTTATATAATGTTTTTAGATCCTGATGATTATTTGGAACTAAAATGCTTGTGAAGAGTG 308
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51.3%; Pred. No. 0.00026;
tive 0; Mismatches 169;
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ORGANISM: Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Ver. 2.1
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US-09-816-028A-26
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Steven Barash
TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 982
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1431 TCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGTTCAACAGATAATACCTT 1490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2251 CCAAACATTGAAAGAATTGAATTCTTAATTATTAATGATGGCTCTACTGATAATAGTCA 2192
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1659 TITAAAAGAATITITAAAAGATAAAACGCTAGCTIGIGITITATACCACTAATA 1711
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                           Length 2406;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diskette, 3.50 inch, 1.4Mb storage
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Pred. No. 0.0028;
1; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <URKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; SEQUENCE DESCRIPTION: SEQ ID NO: 308.
US-09-070-927A-308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
                                                                                                                                                                  Sequence 308, Application US/09070927A Patent No. US20020120116A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 308:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                           APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2406 base pairs
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
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Matches 147; Conservative
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US-09-070-927A-308/c
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1471 GGTTCAACAGATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCCTAGGGTA 1530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1531 CGCATCATGTCTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCCGTTTCTTTT 1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1411 TGTGTAGATAGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGAT 1470
2131 TGGGGGAATTGGAAAAGCCTTTAACTTGGGTGTTTCAGAAGCAAAAGGTGAGTATATTGC 2072
                                                                                                                                                                                                                                          APPLICANT: Chol et. al. TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 GAAACTCTATATAAAAAATAGTAGAGTATCAGGCTGATATTGCAGTTGGTAATTATTAT 301
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                                                                   2071 TGAATTTGAAAGTGACGATTATGTAGCATTGCATGCCTATGACGTTTATACAA 2018
                                         1611 GCAGTTAGATTCAGATGATTATCTTGAGCCTGATGCAGTTGAACTGTGTTTAAA 1664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.0%; Score 60.6; DB 10; Length 44.6%; Pred. No. 0.0046; Live 0; Mismatches 294; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                      Sciences, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; SEQUENCE DESCRIPTION: SEQ ID NO: 199: US-09-765-272-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Human Genome Scier
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                              Sequence 199, Application US/09765272 Patent No. US20020061545A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGIH: 2023 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 199: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                             STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity Matches 237; Conserv
                                                                                                                                               RESULT 13
US-09-765-272-199
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUSCLE AND FOSITION
FILE REPRENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION DATE: 2001-09-24
SEQ ID NOS: 15112
SEQ ID NOS: 15112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2385 TAATAGACTAATAAAAACTGAGGCACATTTAAGTAATATTAATAAATTAAGTCAGTTAAA 2444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2085 TAGAAAGTATATCTTCAATAAAACCGCTGAATATCAAGAAGAAATGGATATGTTAAAAGA 2144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2025 ATTAAATAGACAAGGCATCAATTATTATAATTATGACAAATTTGATGATTTAGATGAAAG 2084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1711 AGAAACGTCAATCCGGATGGTAGCTTAATCGCTAATGGTTACAATTGGCCAGAATTTCA 1770
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                                                                                                                                                                                              1831 TGGCATTTAACGGATGGATTTAACGAAAATATTGAAAACGCCGTGGATTATGACATGTTC
                                                                                               CGAGAAAAACTCACAACGGCTATGATTGCTCACCATTTTAGAATGTTTACGATTAGAGCT
                                                                                                                                         362 AAAGTATATGATAATGTTTCTTTGAGAACTTGTATGAAACTCAAGAAATGAAGAGT
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                                                                                                                                                                                                                                                                                                                 NAME/KEY: unsure

; LOCATION: (76).(90)

OTHER INFORMATION: unsure at all n locations

; OTHER INFORMATION: Clone ID: 25-LIB3057-018-Q1-K1-G1

US-09-960-352-5785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 58.8; DB 10;
Pred. No. 0.0073;
0; Mismatches 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5785, Application US/09960352 Patent No. US20020137139A1 GENERAL INFORMATION:
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Sequence 5558, Application US/09960352

Petent No. US20020137139A1

GENERAL INFORMATION:

APPLICANT: Wasley C.

APPLICANT: Tao, Nengbing

APPLICANT: Wathalagan, Nagappan

TITLE OF INVENTION: MUSCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

TITLE FEFERENCE: 16511.006/37-21(10298)C.

CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 15112

SEQ ID NO 5558

LENGTH: 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2224 AAACTAAACAATATTATTGAATATAAAAAATATATTGTTGTTATTATTCTACATGTTGAT 2283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2404 GAGGCACATTTAAGTAATATAATAAATTAAGTCAGTTAAATCTAAATTGTGAATACATC 2463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.0%; Score 58.6; DB 10; Length 431;
ilarity 47.6%; Pred. No. 0.0076;
Conservative 0; Mismatches 189; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA

ORGANISM: Bos taurus

CTHER INFORMATION: Clone ID: 24-LIB3057-024-Q1-K1-F7

US-09-960-352-5558
                                                       2445 TCTAAATTGTGAATACATCATTTTTGATAATCATGA 2480
                                                                                  94 ATATNAAAACTAACCCTCNATACCTTATTGCCATTA 59
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Job time : 277 secs
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Best Local Similarity
Matches 172; Conserva
                                                                                                                                                      RESULT 15
US-09-960-352-5558/c
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 1, Appli	Sequence 4, Appli	Sequence 3, Appli	Sequence 8, Appl1	Sequence 8, Appl1	æ	Sequence 2, Appl1	Sequence 2, Appl1	Sequence 9, Appl1	Sequence 9, Appli	Sequence 2, Appli	Sequence 2527, Ap	Sequence 2527, Ap	Sequence 2987, Ap	Sequence 137, App	Sequence 137, App	Seguence 6574, Ap	Sequence 2421, Ap	Sequence 3, Appli	Sequence 1938, Ap	Sequence 1, Appli
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GENERAL INFORMATION:
APPLICANT: THE BOARD OF RECENTS OF THE UNIVERSITY OF OKLAHOMA
TITLE OF INVENTION: POLYMER GRAFTING BY POLYSACCHARIDE SYNTHASES
FILE REFERENCE: 617481-5
CURRENT APPLICATION NUMBER: PCT/US99/26501
CURRENT APPLICATION NUMBER: 60/107,929
EARLIER APPLICATION NUMBER: 60/107,929
EARLIER FILING DATE: 1999-11-11
EARLIER FILING DATE: 1999-11-11
EARLIER FILING DATE: 1999-04-01
SOFTWARE: Patentin Ver. 2.0
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GENERAL INPORMATION:
TEREST INPORMATION:
TITLE OF INVENTION: CHONDROITIN SYNTHASE GENE
TITLE OF INVENTION: USING SAME
TITLE OF INVENTION: USING SAME
TITLE OF INVENTION: USING SAME
CURRENT APPLICATION NUMBER: PCT/US01/13395
CURRENT FILING DATE: 2001-04-25
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
SOFTWARE: PATENTION NOWER: 0/199,538
PRIOR FILING DATE: 2000-04-25
SOFTWARE: PATENTION NOWER: 2001-04-25
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Matches 2969;
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                          GAATCATCTTACACCAGACATCAAAAAAAAAATATTGGCTTTCTATCATAAGCAC
                                    AGGCACATTTAAGTAATTAATTAAATTAAGTCAGTTAAATCTAAATTGTGAATAC
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Db 2941 AATAGTATAACGTATAAAACATTTGCATTTTATTAAAA 2979

BESULT 4
US-10-011-768B-8
Sequence 8, Application US/10011768B
Sequence 8, Application US/10011768B
GENERAL INFORMATION:
APPLICANT: DeAngel, Paul H.
APPLICANT: Manari, Kshama
TILLECANT: Knamari, Kshama
TILLECANT: Knamari, Kshama
FILLE REFERENCE: 3554.01
CURRENT FILLING DATE: 2001-12-11
PRIOR FILLING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: US 60/064,435
PRIOR FILING DATE: 1998-10-26
PRIOR RELING DATE: 1998-10-36
PRIOR FILING DATE: 1999-10-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
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          GACATCAAAAAAGAAATATTGGTTTCTATCATAAGCACCAAGTGAATATTTACTAAAT
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APPLICANT: DeAngelis, Paul
APPLICANT: Commari, Kshama
TITLE OF INVENTION: Hyaluronan Synthase Ger
FILE REFERENCE: 3554.011
CURRENT APPLICATION NUMBER: US/10/011,771B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: US 09/178,851
PRIOR PLING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: US 60/064,435
PRIOR FILING DATE: 1997-10-31
NUMBER OF SEQ ID NOS: 10
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US-10-011-771B-8
US-10-011-771B-8
Sequence 8, Application US/10011771B
Sequence 8, Application US/10011771B
Sequence 8, Application Sequence 8, Application Sequence 8, Application Sequence 9, TITLE REPERENCE: S154.01
CURRENT APPLICATION NUMBER: US/10/011, CURRENT FILING DATE: 1998-10-26
PRIOR FILING DATE: 1998-10-26
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NUMBER OF SEQ ID NOS: 10
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                                                                  Length 2937;
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                                                                                      0; Mismatches 375;
                                                                  Score 2285;
Pred. No. 0;
                              TYPE: DNA
ORGANISM: Pastuerella Multocida
3.1
                                                                  Query Match 76.7%;
Best Local Similarity 86.5%;
Matches 2541; Conservative
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<u> </u>	1587	GTTPCTTTTGCTAAGGTTATTACATTGGGCAGTTACATTCACATGATTATCTTGAGCCT 1641 CHIHILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	qq	2641 C
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ð 5	2002	CATTITGTTGTTGTAGTCAATCAGTCATTAAATAGACAAGGCATCAATTATTATAATTATGAC 2061 		CURRENT CURRENT
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ANT: BOATG of Regents of the University of Oklahoma
OF INVENTION: NUCLEIC ACID ENCODING HYALURONAN SYNTHASE AND METHODS
OF INVENTION: OF USE
BEPERENCE: 617022-7
T APPLICATION NUMBER: PCT/US99/07289
T FILING DATE: 1999-04-01
R APPLICATION NUMBER: 60/080,414
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                                                                                      Score 2283.4;
Pred. No. 0;
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EARLIER FILING DATE: 1998-04-02
EARLIER APPLICATION NUMBER: 60/178,851
EARLIER FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
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FILE REFERENCE: 5820.530
CURRENT APPLICATION NUMBER: US/09/283,402
CURRENT FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 2937
TYPE: DNA

ORGANISM:

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                Score 2283.4;
Pred. No. 0;
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US-09-283-402-2
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Sequence 2, Application US/09283402
GENERAL INFORMATION:
APPLICANT: Paul DeAngelis
TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTURELLA
TITLE OF INVENTION: MULTOCIDA AND USES THEREOF

RESULT 7 US-09-283-402-2

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US-09-469-200-2
Sequence 2, Application US/09469200
GENERAL INFORMATION:
APPLICANT: Board of Regents of the
TITLE OF INVENTION: NUCLEIC ACID EN
TITLE OF INVENTION: OF USE
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Regents of the University of Oklahoma NUCLEIC ACID ENCODING HYALURONAN SYNTHASE AND METHODS OF USE

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Pred. No. 0;
0; Mismatches
FILE REFERENCE: 617022-7
CURRENT APPLICATION NUMBER: US/09/469,200
CURRENT FILING DATE: 1999-112-21
PRIOR APPLICATION NUMBER: 60/080,414
PRIOR FILING DATE: 1998-04-02
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/178,851
PRIOR FILING DATE: 1998-10-26
NUMBER OF SED ID NOS: 29
SOFTWARE: PATENTIN Ver: 2.0
SED ID NO 2
LENTH: 2937
                                                                                                   ; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-09-469-200-2
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86.58;
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HYALURONAN SYNTHASE

APPLICANT: Weigel, Paul H
APPLICANT: Weigel, Paul H
APPLICANT: Weigel, Paul H
APPLICANT: Bengells, Paul
APPLICANT: DeAngells, Paul
TITLE OF INVENTION: STREPTOCOCCUS EQUISIMILIS HYA.
TITLE OF INVENTION: IN BACILLUS SUBTILLS
FILE REFERENCE: 3554 .049
CURRENT APPLICATION NUMBER: US/09/879,959
CURRENT FILING DATE: 2001-09-12
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1998-10-26

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2937

; Length Indels

DB 33; 376;

Score 2283.4; Pred. No. 0; 0; Mismatches

76.6%; 86.5%;

Similarity 86.5 0; Conservative

Best Local Sim Matches 2540;

Query Match

pasteurella multocida

) ORGANISM: po US-09-879-959-9

NUMBER OF SEQ ID NOS: 10 SOFTWARE: Patentin version 3.1

2937

SEQ ID NO 9 LENGTH: 29 TYPE: DNA

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Sequence 9, Application US/09879959

RESULT 9 US-09-879-959-9

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2340 1980 2040 2160 2241 2220 2280 2361 2421 2400 2481 2541 2520 2580 2640 2760 1920 2061 2121 2100 2181 2301 2401 ATTAATAAATTAAGTCAGTTAAATCTAAATTGTGAATACATCATTTTTGATAATCATGAC 2460 2601 2661 2721 2700 2781 1941 2001 2841 2761 CAATTTGCACTTTTAATCTTAGAAAAGAAAACCGGCCATGTATTAATAAAACATCGACC 2820 CTGACTTATATGCCTTGGGAACGAAATTACAATGGACAAATGAACAAATTCAAAGTGCA 2901 2821 CTGACTTATATGCCTTGGGAACGAAATTACAATGGACAAATGAACAAATTGAAAGTGCA 2880 AAAAAAGGGAAAATATCCCGTTAACAAGTTCATTATTAATAGTATAACGCTATAA 2958 1921 AACCGTGTATTACATGGTGATAACAATCAATTAAGAAACTTGGCATTCAAAAGAAAAC 2161 GTCAGTATTTTTTATCCCAATACATTAAACGGCTTAGTGAAAAAAACTAAACAATATTTT 2461 AGCCTATTCGTTAAAAATGACAGCTATGCTTATATGAAAAATATGATGTCGGCATGAAT 2062 AAATTTGATGATTTAGATGAAAGTAGAAAGTATATCTTCAATAAAACCGCTGAATATCAA GAAGAAATGGATATGTTAAAAGATCTTAAAACTCATTCAAAATAAAGATGCCAAAATCGCA 2182 GTCAGTATTTCTATCCCAATACATTAAACGGCTTAGTGAAAAAACTAAACAATATTT 2242 GAATATAATAAAAATATATTCGTTATTATTCTACATGTTGATAAGAATCATCTTACACCA ATTAATAAATTAAGTCAGTTAAATCTAAATTGTGAATACATCATTTTTGATAATCATGAC 2482 AGCCTATTCGTTAAAAATGACAGCTATGCTTATATGAAAAAATATGATGTCGGCATGAAT CAATTTGCACTTTTAATCTTAGAAAAGAAAACCGGCCATGTATTTAATAAAAACTGGACC GACATGTTCCTTAAACTCAGTGAAGTTGGAAAATTTAAACATCTTAATAAAATCTGCTAT **AACCGCGTATTACATGGTGATAACACATCCATTAAGAAACTCGGCATTCAAAAGAAAAAC** 2422 2902 2122 2602 2641 2842 1801 1882 1942 2002 2101 2221 2581 2662 2782 94 94 95 Qy Db q QΩ Oy Dp οy q g Q qq g ò 셤 ò g ò QQ 9 0 0 0 g οy qq οy 9 9 9 9 ò οy δý ò

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Pred. No. 0;
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                                                                 GENERAL INFORMATION:
APPLICANT: Weigel, Paul H
APPLICANT: Kumari, Kshama
APPLICANT: Canari, Kshama
APPLICANT: Deangells, Paul
FILECANT: Deangells, Paul
FILE REFERENCE: 3554.048
CURRENT APPLICATION NUMBER: US/10/172,527
CURRENT APPLICATION NUMBER: 60/297,788
PRIOR APPLICATION NUMBER: 60/297,788
PRIOR PILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VETSION 3:1
SEQ ID NO 9:
                                                 Sequence 9, Application US/10172527
                                                                                                                                                                                                                                                                             ; ORGANISM: pasteurella multocida US-10-172-527-9
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Conservative
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                                                           GENERAL INFORMATION:
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Best Local Simi
Matches 2540;
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SOFTWARE: Patentin Ver. 2.0
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Sequence 2, Application PC/TUS9926501
Sequence 2, Application:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: POLYMER GRAFTING BY POLYSACCHARIDE SYNTHASES
FILE REPERENCE: 617481-5
CURRENT APPLICATION NUMBER: 60/107,929
EARLIER APPLICATION NUMBER: 60/107,929
EARLIER APPLICATION NUMBER: 60/107,929
EARLIER APPLICATION NUMBER: 09/283,402
EARLIER PILING DATE: 1999-11-11
EARLIER FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 6
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Pred. No. 2.9e-273;
0; Mismatches 348;
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Best Local Similarity 82.5%;
Matches 1743; Conservative
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APPLICATION NUMBER: US/09/107,532
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GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REPERENCE,DOCKET NUMBER: GTC-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEPRAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             085598
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0855
FILING DATE: May 14, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/05157
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Massachusetts
. USA
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2101 AAAGATATTTAA 2112
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-09-107-532-2527
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Matches 181; Conservative
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Best Local Similarity 54.0
Matches 176; Conservative
                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-107-532A-2527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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US-09-107-532A-527
US-09-107-532A-527
Sequence 2527 Application US/09107532A
GENERAL INFGRAMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
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                                                                                                                                                                                                                                                                                                                               Length 984;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                             Query Match 3.0%; Score 89.2; DB 15; Best Local Similarity 54.2%; Pred. No. 1.3e-06; Matches 181; Conservative 0; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1649 TTGAACTGTGTTTAAAAGAATTTTTAAAAGATAA 1682
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APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 ATGAAATTTTGTATGAGAATTTGAAAATTCATGA 347
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
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OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                      ORGANISM: Enterococcus faecium
                                                                                                 TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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                                  LENGTH: 984 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                             ) NAME/KEY: misc_feature
; LOCATION: 1...984
US-09-107-532-2527
INFORMATION FOR SEQ ID NO:
                 SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                            FEATURE:
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Sequence 2987, Application US/09134000A

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS
TITLE OF INVENTION: FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,000A
CURRENT FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 6810
SEQ ID NO 2987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254 TIGCGAGAGGCAAATACTIAGGCTIIGIIGACAGIGAIGAITAIATIGAIGAAGAIATGI 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 ATATAATGTGTGAGATTAGTATTATTGTTCCTGTGTATAAAGTTGAAAAATATTTAAGAA 73
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Pred. No. 5.3e-06;
0; Mismatches 150; Indels
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Pred. No. 1.3e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...984
SEQUENCE DESCRIPTION: SEQ ID NO: 2527:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Enterococcus faecium
                                                                                                        TELEPHONE: (781)893-5007
TELEPAK: (781)893-8277
INFORMATION FOR SEQ ID NO: 2527:
SEQUENCE CHARACTERISTICS:
LENGTH: 984 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                               TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
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US-09-134-000-2987
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Similarity 54.2%;
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                                                                    GTAGATAGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGT 1473
1354 ATACCTTTAGTTTCTATTATATCCCCGCTTATAACTGTGCAAATTATATTCAAAGATGT 1413
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                          139 TCTCCAGACAGTTCTGGAGCAATGTGTGATCAGTTTGCTGAACAAGATCAACGGGTAAAA 198
                                                                                                                                                                                                                                 APPLICANT: Charles Kunsch
APPLICANT: Charles Kunsch
APPLICANT: Patrick J. Dillon
APPLICANT: Steven C. Barash
TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 982
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Communication
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 9410 Key West Avenue CITY: Rockville STATE: Marvland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927
FILING DATE: herewith
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                                                                                                                                                                                                                                                                                                                                                                                         CTATTATATACAAATATCGTAAAAGA 344
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GENERAL INFORMATION:
APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEFAN: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: A. Anders Brookes REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 5550 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 54.0
Matches 176; Conservative
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APPLICATION NUMBER:
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US-09-070-927-137
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US-09-070-927-137
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1594 AAAGGTTATTACATTGGGCAGTTAGATTCAGATGATTATCTTGAGCCTGATGCAGTTGAA 1653
                  1474 TCAACAGATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCCTAGGGTACGC 1533
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ATACCTTTAGTTTCTATTTATATCCCCGCTTATAACTGTGCAAATTATATTCAAAGATGT
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33. /cgn2_6/ptodata/2/pna/USO3_NEW_COMB.seq:*

43. /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

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Sequence 1, Application US/09842484A
GENERAL INFORMATION:
APPLICANT: DEANGELIS, PAUL L.
TITLE OF INVENTION: CHONDROITIN SYNTHASE GENE AND METHODS OF MAKING AND USING SAMI FILLS OF INVENTION: CHONDROITIN SYNTHASE GENE AND METHODS OF MAKING AND USING SAMI FILLS REPERENCE: 4609.003
CURRENT APPLICATION NUMBER: US/09/842,484A
CURRENT FILLING DATE: 2000-04-25
PRIOR FILLING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VEFSION 3.1
SEQ ID NO 1
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APPLICANT: BOANGELIS, Paul
APPLICANT: Bunari, Kshama
TITLE OF INVENTION: Hyaluronan Synthase Gene and
FILE REFERENCE: 3554.011
CURRENT APPLICATION NUMBER: US/09/469,200D
CURRENT APPLICATION NUMBER: US/09/469,200D
PRIOR PILING DATE: 1999-12-21
PRIOR FILING DATE: 1998-10-26
PRIOR FILING DATE: 1998-10-36
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
SOFTWARE: PALCATION NUMBER: US 60/064,435
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PALCATION NUMBER: SECOND SOFTWARE: PALCATION NUMBER: US 60/064,435
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Pred. No. 0;
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; GENERAL INFORMATION:
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US-09-469-200D-8
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Best Local Similarity 86.5%;
Matches 2541; Conservative C
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1641 1620 1680 1761 1740 1860 2040 2121 2160 2241 2280 1401 1461 1521 1500 1581 1701 1881 2001 2061 2181 2301 2421 ACCACTAATAGAAACGTCAATCCGGATGGTAGCTTAATCGCTAATGGTTACAATTGGCCA CCTAGGGTACGCATCATGTCTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCCGCC GTTTCTTTTGCTAAAGGTTATTACATTGGGCAGTTAGATTCAGATGATTATTTTTGGCT GAATTTTCACGAGAAAACTCACAACGGCTATGATTGCTCACCACTTTAGAATGTTCACG AATGACATCTCATATTACACGAGTAATAGACTAATAAAAACTGAGGCACATTTAAGTAAT TGTAACGATGCTTCAACAGATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAAT CCTAGGGTACGCATCATGTCTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCC GTTTCTTTTGCTAAAGGTTATTACATTGGGCAGTTAGATTCAGATTATCTTGAGCCT GAATTTTCACGAGAAAACTCACACACGGCTATGATTGCTCACCATTTTAGAATGTTTACG **ATTAGAGCTTGGCATTTAACGGATGGATTTAACGAAAATATTGAAAACGCCGTGGATTAT** GAATTTGATGATTAGATGAAGTAGAAAGTATATTTTCAATAAAACCGCTGAATATCAA GTCAGTATTTTCTATCCCAATACATTAAACGGCTTAGTGAAAAAAACTAAACAATATTATT GAATATAATAAAAATATATTCGTTATTATTCTACATGTTGATAAGAATCATCTTACACCA **ATTCAAAGATGTGTAGATAGTGCTCTTAATCAAACTGTTGTGGATCTCGAGGTTTGTÁTT** 1762 1942 2062 2302 1261 1342 1321 1402 1381 1462 1441 1522 1582 1561 1642 1621 1702 1681 1741 1822 1801 1882 1861 1921 2002 1981 2101 2182 2161 2242 2221 2281 2362 1501 οy Dp q QQ g ò qq ò qq ò g δ qq g g & qq ò g ò 셤 οy g ò g g õ g οχ οy οy δý ò ò ô

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APPLICANT: WEIGEL, PAUL H
APPLICANT: WINGHI, KSHAMA
TITLE OF INVENTIONS HYALLORONAN SYNTHASES AND METHODS OF MAKING AND USING STILE REFERENCE: 35541.082
CURRENT APPLICATION NUMBER: US/10/309,560
CURRENT FILING DATE: 2002-12-03
PRIOR PELICATION NUMBER: 60/336,105
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patentin version 3.1
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AATGATATCTCATATTACACGAGTAATAGATTAATAAAAACTGAGGCGCATTTAAGTAAT
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                                                            AGCCTATTCGTTAAAAATGACAGCTATGCTTATATGAAAAAATATGATGTCGGCATGAAT
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Pred. No. 0;
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CRGANISM: Pasteurella multocida
US-10-309-560-7
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Best Local Similarity 86.5%;
Matches 2540; Conservative
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                                                                              ATTAATAAATTAAGTCAGTTAAATCTAAATTGTGAATACATCATTTTTGATAATCATGAC
                                                                     AGCCTATTCGTTAAAAATGACAGCTATGCTTATATGAAAAAATATGATGTCGGCATGAAT
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Pred. No. 0;
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GENERAL INFORMATION:
APPLICANT: DEANGELIS, PAUL
TITLE OF INVENTION: DAR ENCODING HYALURO);
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 35541.081
CURRENT APPLICATION NUMBER: US/10/217,61:
CURRENT FILING DATE: 2002-08-12
PRIOR PILLING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/283,402
PRIOR PILLING DATE: 1998-04-02
PRIOR PILLING DATE: 1998-04-02
PRIOR FILING DATE: 1998-04-02
PRIOR FILING DATE: 1998-04-02
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATCHING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 9
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TYPE: DNA
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GAACGAAAATTACAATGGACAAATGAACAAATTGAAAGTGCAAAAAGGGGGGAAAATATA 2880
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APPLICANT: SUGIURA, NOBUO
APPLICANT: SUGIURA, NOBUO
APPLICANT: SUGIURA, NOBUO
TITLE ON INVERTION CHOMPROITIN POLYMERASE AND DNA ENCODING THE SAME
FILE REFERENCE: 226882USO
CURRENT APPLICATION NUMBER: US/10/216,289
CURRENT PILING DATE: 2001-21-04
PRIOR APPLICATION NUMBER: JP 2001-324127
PRIOR FILING DATE: 2001-00-32
PRIOR FILING DATE: 2001-02
PRIOR FILING DATE: 2001-02
PRIOR FILING DATE: 2001-02
PRIOR FILING DATE: 2001-02
PRIOR FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
                   2401 TTAAATCTAAATTGTGAATACATCATTTTTGATAATCATGACAGCCTATTCGTTAAAAT
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                                                                 Sequence 3, Application US/10216289 GENERAL INFORMATION:
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NAME/KEY: CDS
LOCATION: (3787)..(5847)
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LENGTH: 14483
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 Length 14483;
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Score 814.2; DB 6;
Pred. No. 1.6e-146;
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Matches 1312; Conserv
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                        ; General involution;
APPLICANT: NINOMIYA, TOSHIO
APPLICANT: SUGIDRA, NOBUO
APPLICANT: SUGIDRA, NOBUO
TITLE OF INVENTION: CHONDROITIN POLYMERASE AND DNA ENCODING THE SAME
TITLE OF INVENTION: CHONDROITIN POLYMERASE AND DNA ENCODING THE SAME
FILE REPERENCE: 226882U50
CURRENT APPLICATION NUMBER: US/10/216,289
CURRENT PAPLICATION NUMBER: JP 2001-244685
PRIOR PILING DATE: 2001-08-10
PRIOR PILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-20
PRIOR PILING DATE: 2001-0-22
PRIOR PILING DATE: 2001-0-22
PRIOR PILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
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Pred. No. 3.1e-145;
0; Mismatches 743;
Sequence 1, Application US/10216289 GENERAL INFORMATION:
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63.2%;
                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Escherichia coli
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Matches 1296; Conservative
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LOCATION: (1)
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533 TATACGACTATGAAGTTATTGTTGCCGATGAAGTAAAGAAAATATTGAAGAAATAG
                    TGCAAAAATACGAACAAAAACTTGACATAAAGTATGTAAGACAAAAAGATTATGGATATC
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TAATCGCTAATGGTTACAATTGGCCAGAATTTTCACGAGAAAACTCACAACGGCTATGA 1795
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                          AGAAACTCGGCATTCAAAAGAAAACCATTTGTTGTTGTAGTCAATCAGTCATTAAATAGAC
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACI
TITLE OF INVENTION: BATHEROCCCUS FAECALIS FOR
FILLE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SEQ ID NO 2987
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US-09-134-000C-2987
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APPLICANT: Gilbert, Michel
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CURRENT APPLICATION NUMBER: US/02/816,028
PRIOR PILING DATE: 2002-11-21
PRIOR PLILING DATE: 1999-02-01
PRIOR PLILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.1
SED ID NO 14.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: 11.5 kb PCR product from C. jejuni OH4384; OTHER INFORMATION: including LOS biosynthesis locus US-10-303-161-1
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                                                                                                                                                                                     Wakarchuk, Warren W.
National Research Council of Canada
1654 CTGTGTTTAAAAGAATTTTTAAAAGA 1679
                                   319 CTATTATATACAAATATCGTAAAAGA 344
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                                                                                                                            Sequence 1, Application US/10303161
GENERAL INFORMATION:
APPLICANT: Gilbert, Michel
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ORGANISM: Campylobacter jejuni
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US-10-303-162-1/c
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APPLICANT: Wakarchuk, Warren W.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Blosynthesis of
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Blosynthesis of
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Blosynthesis of
TITLE REFERENCE: 019633-0001110S
CURRENT APPLICATION NUMBER: US/10/303,162
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/118,213
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
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CURRENT APPLICATION NUMBER: US/10/303,118
PRIOR FILING DATE: 2001-01-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 1999-02-01
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US-10-303-128-1
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                                                                                                                                                                                                                                                                                                                                                                                                                    Length 11474;
                                                                                                                                                                                                                                                                                     OTHER INFORMATION: 11.5 kb PCR product from C. jejuni OH4384 OTHER INFORMATION: including LOS biosynthesis locus
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PRIOR APPLICATION NUMBER: US 09/495,406
                                                                                                                                                                                        TYPE: DNA
ORGANISM: Campylobacter jejuni
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                                 PRIOR FILING DATE: 2000-01-31
                                                     NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.1
                                                                                                                     SEQ ID NO 1
LENGTH: 11474
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Sequence 1, Application US/10303134

GENERAL INFORMATION:
APPLICANT: Glibert, Michel
APPLICANT: Makarchuk, Warren W.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
FILE REFERENCE: 019633-00011US
CURRENT APPLICATION NUMBER: US/10/303,134
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 2000-01-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11184 CTTTCAAAATGAAGAAAATTTAGGCACTTTTGCAAGTAGAAATTTGGGGGTTTTGCATTC
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      Length 11474;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.7%; Score 79.2; DB 6; Length 1 Best Local Similarity 51.2%; Pred. No. 1.8e-06; Matches 211; Conservative 0; Mismatches 198; Indels
   Score 79.2; DB 6;
Pred. No. 1.8e-06;
                                                               0; Mismatches
                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Campylobacter jejuni
2.7%;
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SOFTWARE: Patentin Ver. 2.1
                                                               Conservative
                                 Similarity
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LENGTH: 11474
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                                                               Matches 211;
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                                                                                                                                                                                                                                                                                                11184 CTTTCAAAATGAAAAATTTAGGCACTTTTGCAAGTAGAAATTTGGGGGTTTTGCATTC 11125
11364 GCCACAACTITCTAICATAATCCCGCTITITAATTCTTGCGATTITATCTCAAGAGCTIT 11305
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                                                                                                              11304 GCAAAGTTGTATAAATCAGACTTTAAAAGATATTGAAATTTTGATTATCGATGATAAAAG
                                                                                                                                                                                           1536 CAT---GICTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCCGTTTCTTTGC
                                                                   1416 AGATAGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGTTC
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pred. No. 4.3e-06;
0; Mismatches 543;
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US-10-240434-27.

SQUEGRAL INFORMATION:

APPLICANT: OLEK, Alexander

APPLICANT: OLEK, Alexander

APPLICANT: DIEBENBROCK, Christian

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Asseries Reference: 5013.1010

CURRENT FILING DATE: 2002-10-02

CURRENT FILING DATE: 2002-10-02

PRIOR PILING DATE: 2001-04-06

PRIOR PILING DATE: 2001-04-06

PRIOR PILING DATE: 2000-04-06

PRIOR PILING DATE: 2000-04-06

PRIOR PILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR PILING DATE: 2000-06-07

PRIOR PILING DATE: 2000-06-07

PRIOR PILING DATE: 2000-06-10

PRIOR PILING DATE: 2000-06-30

PRIOR PILING DATE: 2000-06-30

PRIOR PILING DATE: 2000-06-30

PRIOR PILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 68

SEQ ID NO 27

SEQ ID NO 27

SEQ ID NOS: 68
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Best Local Similarity 43.9%;
Matches 434; Conservative (
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16107 TATCCCTATTAAAAATCAAAACTATCTCTCATATATTCCTTCAAACATAACTATAAATTA 16048
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                                                                                                       AAAAAAAATAAAAAAAAAAAACCAACAAAAAAAAAAACCAACCAACACCTCTTAAAAC 16641
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                        TTTACTAAATAATGACATGTCATATTACACGAGTAATAGACTAATAAAAACTGAGGCACA 2411
CAATATTATTGAATATAAAAAAAATATATTCGTTATTATTATTCTACATGTTGATAAGAATCA 2291
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                                                                       TCTTACACCAGACATCAAAAAAAAATATTGGCTTTCTATCATAAGCACCAAGTGAATAT
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APPLICANT: Havukkala, Ilkka J
APPLICANT: Havukkala, Ilkka J
APPLICANT: Havukkala, Ilkka J
APPLICANT: Lubbers, Mark William
APPLICANT: Lubbers, James
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: them, and methods for using them.
FILE REFERENCE: 11000.1043c3
CURRENT APPLICATION NUMBER: US/10/264,213
CURRENT FILING DATE: 2002-10-03
NUMBER OF SEQ. ID NOS: 253
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16047 CAAAATATTATCCCAATTTTATAACA 16020
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LENGTH: 13825
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US-10-264-213-27

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                                                                                               Qy 1354 ATACCTTTAGTTTCTATTATATCCCCGCTTATAACTGTGCAAATTATATTCAAAGATGT 1413
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                                                        Gaps
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Query Match

2.6%; Score 76.6; DB 6; Length 13825;
Best Local Similarity 53.5%; Pred. No. 5.6e-06;
Matches 160; Conservative 0; Mismatches 139; Indels 0;
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Job time : 319 secs
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BEST AVAILABLE GORY

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Title: Perfect score:

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Scoring table:

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Genoscope.

Direct Submission

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDCP is constructing a physical map of the Drosophila melanogaster genome.using these BACs. For further information please see http://www.fruifiy.org The BDCP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster genome survey sequence T7 end of BAC:
BACKS9B23 of RPCI-98 library from Drosophila melanogaster (fruit AL069706
                                                                                                                                   ALO61936 Drosophil
ALO6363 Drosophil
ALO63921 Drosophil
ALO63921 Drosophil
ALO63921 Drosophil
ALO6392 Drosophil
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BLILO2 F19C22-T7 I
ALA3638 Tetracdon
ALO6344 Drosophil
ALO6344 Drosophil
ALO6342 Tetracdon
ALO63921 Drosophil
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ALO63938 ENTKROTF
ALZ26115 Tetracdon
ALO63921 Drosophil
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ALO63948 DROSOPHIL
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BOB76453 AGBNCOURT
AL419462 T3 end of
BG854775 1024040G1
BF272396 GA_EB001
AZ53976B ENTDC17TR
AL106171 Drosophil
AL229840 Tetracdon
AL071865 Drosophil
BM416130 OP21217 M
                                                        AL298972 Tetraodon
BG850019 1024027H0
AG058583 Pan trog1
BH391984 AG-ND-138
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CNSO029G
AL514901
CNSO167M
CNSO18BG
B11102
CNSO7ABZ
CNSO7ABZ
CNSO09DO
AZ662338
CNSO030G
CNSO13GG
CNSO13GG
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AY068550
CNSO13GG
AY06850
CNSO13GG
AY075GG
AY06850
CNSO13GG
AY06850
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CNS0161D
CNS035N7
CNS00DKY
BM416130
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AG058583
BH391984
CNS0021J
CNS0155H
CNS010B8
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Drosophila melanogaster
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CNSO0EVL
LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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TITLE
JOURNAL
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                                                                                                                                     January 3, 2003, 21:14:45; Search time 3682 Seconds
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                    GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Database

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BM415636 CNS00FUH AQ946120 BI815821 CNS020K7

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the potato cyst
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EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                          others
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                                                                                   /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACK29B23"
/clone_lib="RPCI-98"
/note="end : T7"
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al Similarity 34.3%; Pred. No. 4.7e-
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'/organism="Globodera pallida"
'/db_xref="taxon:36090"
'/db_xref="taxon:36090"
'/db_xref="taxon:36090"
'/dlone_lib="Mixed Stage EST's from Globodera pallida, the potato cyst nematode"
'/orde="voctor: lambda GT11; This is a collaborative effort between IACR-Rothamsted and North Carolina State University. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs,
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                                               1 (bases 1 to 910)
Her,J., Sosinski,B., Pokrzywa,R.M., Warry,A. and Opperman,C. Mixed Stage EST's from Globodera pallida, the potato cyst nematode Oppublished (2001)
                        Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
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                                         Tylencholdea; Heteroderidae; Heteroderinae; Globodera
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                                                                                                                                         Contact: Opperman, C
Center for the Biology of Nematode Parasitism
NC State University; IACR-Rothamsted
Campus Box 7616; Raleigh, NC 27695, USA
Fax: 919.515.6699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 86.8; DB 13;
Pred. No. 8.8e-07;
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                                                                                                                                                                                                                                              Email: warthog@unity.ncsu.edu
GT11-6PCN_F_D07_PCN_6_F_058.abl.
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Listed (10-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr

- Wab : www.genoscope.cns.fr)

- Wab : www.genoscope.cns.fr)

- Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDCP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDCP Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDCP Drosophila melanogaster genome using these PACs. For further information please see http://www.fruitfly.org The BDCP Drosophila melanogaster and plarary was prepared by Kazutoyo Oscogawa and Aaron Mammoser in Pieter de Jon's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1.98 and was constructed by partial isogenic strain v2; cn bw sp, the same strain used for the BDGP's pland by to order indyvidual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://Pacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                    Jy6 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR31021 of RPCI-98 library from Drosophila melanogaster (fruit AL0)1063
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                                                                     |:| :| |||::| :| |||: |||: ||| : |||| : |||| |||||: ||||: ||||: |||: |||: ||||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: 
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                                  Drosophila melanogaster.
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                       AAATACGAACAAAAACTTGACATAAAGTATGTAAGACAAAAAGATTATGGATATCAA 717
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/db_xref="taxon:7227"
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/note="end : TET3"
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/organism="Trypanosoma bruce;"
/strain="Trypanosoma bruce;"
/strain="Trypanosoma bruce;"
/db_rafe="Trypanosom:5691"
/clone="Sheared DNA-46J23"
/clone="Sheared DNA-46J23"
/clone="Sheared DNA-46J23"
/clone="Sheared DNA-46J23"
/clone="Sheared DNA-8516_1: Smal; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma bruce; (TREU92//4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + 1 method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing; A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sheared DNA-46J23.TR Sheared DNA 11near GSS 27-JAN-2000
Sheared DNA-46J23, DNA sequence.
Sheared DNA-46J23, DNA sequence.
AQ946120
AQ946120.1 GI:6769385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Fraser,C. and Adams,M.
Determination of clone end sequences from Trypanosoma brucei GUTat
10.1 sheared DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared DNA library constructed at TIGR. Clones will be available for distribution through ATCC. Sheared DNA end sequences search page: http://www.tigr.org/tdb/mdb/tbdb/. Seq primer: Ml3.Reverse Class: shotgun.
ACACGAGTAATAGACTAATAAAAACTGAGGCACATTTAAGTAATATTAATAAATTAAGTC 2437
                                                                                                                                AGTTAAATCTAAATTGTGAATACATCATTTTTGATAATCATGACAGCCTATTCGTTAAAA 2497
                                                                                                                                                                                                                                                                     ATGACAGCTATGCTTATATGAAAAATATGATGTCGGCATGAATTTCTCAGCATTAACAC 2557
                                                                                                                                                                                                                                                                                                                                                                                                             ATGATTGGATCGAGAAAATCAATGCGCATCCACCATTTAAAAAGCTGATTAAAAACCTATT 2617
                                                                TITITITITITITYYCCSSSCSCSCSSCCVAAAVAAATTAWWAAIKTWATWTWAWITIT 958
                                                                                                                                                                                                                                                                                                        Trýpanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MD 20850, USA
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Other_GSSs: Sheared DNA-46J23.TF
Ochter_TSSs: Sheared DNA-46J23.TF
Cortect: Najlb M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2618 TTAATGACAATGACTTAAGAAGTATGAA 2645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KWAATWAWAAAAWATTTTTTTTATWAA 986
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1 (bases 1 to 641)
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/organism="Plasmodium falciparuum"
/db_xref="taxon:5833"
/db_xref="taxon:5833"
/clone_lib="labamodium falciparuum 3D7 asexual cDNA"
/lab_host="bull0B (GeneHoy, Invitrogen, Inc.):
/note="vector: pBluescript SK plus; Site_1: EcoRI; Site_2:
/note="vector: pBluescript SK plus; Site_2: Eagering Structed by A+ RNA was isolated by the polyA+ Tract
mRNA isolation system (Promega, WI) using streptavidin
/note EcoRI and Xho! sites of 1 ZapII vector using the Zap
/constructed by oligo d(T) priming of poly(A)+ RNA (Smg)
/into EcoRI and Xho! sites of 1 ZapII vector using the Zap
/clones were mass excised using the ExAssist helper phage
/clones were mass excised using the ExAssist helper phage
/swas electroporated with phenol/chloroform. Phagemid DNA
/was electroporated into hHobe cells:"
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                                                                                                                                                                                                                                 Email: estewatson.wustl.edu
Library was constructed by Debopam Chakrabarti DNA
Washington University Genome Sequencing Center For
obtaining a clone please contact: L. David Sibley
(sibley@borcim.wustl.edu), Washington University
Seq primer: -400P from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 80; DB 13;
Pred. No. 1.9e-05;
Unpublished (2001)
Contact: L. David Sibley
WashU Plasmodium EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 431.
Location/Qualifiers
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nilarity 47.4%; E
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314 286 1810
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Matches 239;
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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169 c 165 g 262 t 113 others
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; Pred. No. 3e-05;
58; Mismatches 227; Indels 0;
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Understood Sequence of Sequence of Sequences of Submitted (02-JUN-1999) Genoscope - Centre National de Sequences of Submitted (02-JUN-1999) Genoscope - Centre National de Sequences of BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-99 and was constructed by partial Ecor I digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pland EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster genome survey sequence T7 end of BAC:
BACKS9B23 of RPCI-98 library from Drosophila melanogaster (fruit AL069706
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2429 AATTAAGTCAGTTAAATCTAAATTGTGAATACATCATTTTTGATAATCATGACAGCCTAT 2488
                                                                                                                                                                                                                                                                                          2549 CATTAACACATGATTGGATCGAGAAAATCAATGCGCATCCACCATTTAAAAAGCTGATTA 2608
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                               TCGTTAAAAATGACAGCTATGCTTATATGAAAAATATGATGTCGGCATGAATTTCTCAG
                                                                                                                                                                                             Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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/clone_lib="RPCI-98"
/note="end : T7"
91 c 60 g
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CNSO6KHQ 1169 bp DNA linear GSS 17-JUN-2U1 T3 end of clone ATOAA005D05 of library ATOAA from strain CBS 4311 of Saccharomyces servazzii, genomic survey sequence.
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Saccharomyces servazzii
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2317 ATATTGGCTTTCTATCATAAGCACCAAGTGAATATTTTACTAAATAATGACATCTCATAT 2376
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                                                                                                                                        TGTTTAAAAGAATTTTTAAAAGATAAAACGCTAGCTTGTGTTTATACCACTAATAGAAAC 1716
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/plasmid="pBeloBAC11"
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                 /note="end : T7
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37.1%;
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289; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk · This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                              2246 ATAATAAAAATATTCGTTATTATTCTACATGTTGATAAGAATCATCTTACACCAGACA 2305
                                                                                                                                                                                                                                                                                                                                                               2306 TCAAAAAAGAAATATTGGCTTTCTATCATAAGCACCAAGTGAATATTTACTAAATAATG 2365
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      TIWIAAAAIAIAWWIIAAIAAAAIAIAIWIAWIAWWAIAIAIAWAAIAWAAWIAIAWAWIWW 970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2426 ATAAATTAAGTCAGTTAAATCTAAATTGTGAATACATCATTTTTGATAATCATGACAGCC
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                                                                                                                                                                                      TTGATGATTTAGATGAAAGTAGAAGTATATCTTCAATAAAACCGCTGAATATCAAGAAG
                                                                                                                              2126 AAATGGATATGTTAAAAGATCTTAAACTCATTCAAAATAAAGATGCCAAAATCGCAGTCA
                                                                                                                                                                                                                                   TATTCGTTAAAAATGACAGCTATGCTTATATGAAAAAATATGATGTCGG 2534
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/db_xref="texon:7227"
/clone="BACW01115"
/clone_lib="DrosBAC"
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Genoscope

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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              994 bp DNA linear GSS 21-MAY-2000 nigroviridis genome survey sequence T7 end of clone library G from Tetraodon nigroviridis, genomic survey.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tetraodontidae; Tetraodon.

( Loases 1 to 94)

Roest-Crollius, Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.

Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
Uppbblished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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                                                                                                                                                                                                                                                                                        783 TATTTAT-ATAAAAAWAAAAAAAAAWATAAATTTTATAAATTATAAAAANATATATT
                                                                                                                                                                    GAATATTTTACTAAATAATGACATCTCATATTACACGAGTAATAGACTAATAAAAACTGA
                                                                      2286 GAATCATCTTACACCAGACATCAAAAAGAAATATTGGCTTTCTATCATAAGCACCAAGT
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/db_xref="taxon:99883"
/clone="122P04"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRR cedex, FRANCE. (E-mail: Sequefégenoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces extaguus, Saccharomyces servazil, 29posaccharomyces rouxil.
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                                Jouciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bouciet, J.L., Aigle, M., Bon, E., Brottier, P., Casaregola, S., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., Bolotin, B., Dubrens, P., Lepilagle, A., Liorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, M., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
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FEBS Lett. 487 (1), 47-51 (2000)
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iive 26; Mismatches 294; Indels 4;
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McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants; project phase 2
Unpublished (2000)
Contact: Charles Hauser
DCMB Hox 91000
Duke University
Duke University
Durham, NO 27708-1000
Tel: 919 613 8159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 973;
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                                                                                                                                                                                                          /organism="Chlamydomonas reinhardtii"
                                                                                                                                                                                                                      /strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
                                                                                                                                                                                                                                                 /clone_lib="C. reinhardtii CC-1690,
II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 76.4; DB 12;
Pred. No. 8.7e-05;
0; Mismatches 291;
                                                                                                                                                                     Location/Qualifiers
1. .973
                                                                                                                                                                    chauser@duke.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.68;
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Query Match
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Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission
Submitted (02-AUG-2001) Asso Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-Chou, Fsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mall:Chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:i8145-503-9111, Pax:81-45-503-9170)

Tel:als 145-503-9111, Pax:81-45-503-9170)

Was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                         Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-045107.F.
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                        GSS 02-NOV-2001
                                                                                                                                                        778 bp DNA linear GSS 02-NOV-200 clone: PTB-045107.F, genomic survey sequence.
                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 17; Length 778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
19 c 64 g 130 t 29 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-045107.F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                         Pan troglodytes DNA,
AG058583
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                                2512 TATATGAAAAATA 2525
                                                                  ATTATAATATAAA 286
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AG-ND-138G17.TR ND-TAM Anopheles gambiae genomic clone AG-ND-138G17
BH391984
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Other_GSSs: AG-ND-138G17.TF.1
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
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This clone is from an A. gambiae BAC library (ND-TAM) provided by
This clone is from an A. gambiae BAC library (ND-TAM) provided by
The Clone is from a sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
2275 CATGTTGATAAGAATCATCTTACACCAGACATCAAAAAAGAAATATTGGCTTTCTATCAT 2334
                                                                                                                                                                                                                           AAGCACCAAGTGAATATTTACTAAATAATGACATCTCATATTACACGAGTAATAGACTA 2394
                                                                                                                                                                                                                                                                                                                                        ATAAAAACTGAGGCACATTTAAGTAATATTAATAAATTAAG---TCAGTTAAATCTAAAT 2451
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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46.1%; Pred. No. 0.00011;
Live 0; Mismatches 340; Indels
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277 t

    .832
    /organism="Anopheles gambiae"

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/clone_lib="ND-TAM"
/note="Vector: pECBAC3
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/db_xref="taxon:7165"
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Seq primer: M13 Rev
Class: BAC ends.
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Drosophila melanogaster genome survey sequence TET3 end of BAC # BACROSNII of RPCI-98 library from Drosophila melanogaster (fruit ILY), genomic survey sequence.
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rmination of this BAC-end sequence was carried out as part of a boration with the Berkeley Drosophila Genome Project (BDGP).
BDGP is constructing a physical map of the Drosophila nogaster genome using these BACs. For further information se see http://www.fruitfly.org The BDGP Drosophila nogaster BAC ibrary was prepared by Kazutoyo Osoegawa and m Mammoser in Pieter de Jong's laboratory in the Department of er Genetics at the Roswell Park Cancer Institute in Buffalo, The library is named RPCI-98 and was constructed by partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ct Submission
itted (02-JUN-1999) Genoscope - Centre National de Sequencage
91 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                               2275 CATGITGATAGAAICAT --- CITACACCAGACATCAAAAAAAGAAATATIGGCITICIA 2330
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                                          AAGAAACTCGGCATTCAAAAGAAAAACCATTTTGTTGTAGTCAATCAGTCATTAAATAGA 2034
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidaa; Drosophilidae; Drosophila.
2331 TCATAAGCACCAAGTGAATATTTTACTAAATAATGACATCTCATATTACACGAGTAATAG
                                                                                                         CAAGGCATCAATTATTATAATTATGACAAATTTGATGATTTAGATGAAAGTAGAAAGTAT
                                                                                                                                                                         ATCTTCAATAAAACCGCTGAATATCAAGAAGAAATGGATATGTTAAAAGATCTTAAAACTC
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                                                                                                                                        ATTCAAAATAAAGATGCCAAAATCGCAGTCAGTATTTTCTATCCCAATACATTAAAACGG
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EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                         melanogaster"
                                                                                                                                                                                                                                     40; Mismatches 405;
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40.1%; Pred. No.
                                                                                                         /organism="Drosophila m
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Drosophila melanogaster genome survey sequence SP6 end of BAC BACN13C23 of DrosBAC library from Drosophila melanogaster (fruit AL1950.2 AL105023.1 GI:5617037
                                                                                                                                                                                                                                                                                                                                                                                      Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.ut. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ξ,
                                                                                                                                                                                                                                                                                                                                             Submitted (23-UUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2048 ATTATAATTATGACAAATTTGATGATTTAGATGAAAGTAGAAAGTATATCTTCAATAAAA 2107
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
Genoscope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Drosophila melanogaster"
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/plasmid="pBeloBAC11"
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Search completed: January 4, 2003, 00:35:28 Job time: 3720 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

January 4, 2003, 00:35:34; Search time 118 Seconds (without alignments) 1089.719 Million cell updates/sec Run on:

US-09-842-484A-2 5089 1 MNTLSQAIKAYNSNDYELAL......SAKKGENIPVNKFIINSITL 965 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 seqs, 133250620 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_101002: Database :

| SIDS2/gcgdata/geneseqp-emb1/Aa1980.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result		Query				
NO.	Score	Match	Match Length DB	DB	ID	Description
			:	-		
-	5089	100.0	-	21	AAY96213	P. multocida chond
7	5089	100.0		23	AAM47335	Pasteurella multoc
٣	5067		-	23	AAM47336	Pasteurella multoc
4	4486.5		-	20	AAY06212	Pasteurella multoc
S	4486.5			21	AAY43099	P. multocida hyalu
9	3079		-	21	AAY96212	P. multocida hyalu
7	292.5			23	ABB48565	Listeria monocytog
80	276.5	5.4	106	22	AAU33454	Enterococcus faeca
9	276.5		-	22	AAU34918	Enterococcus faeca
10	253			23	ABP26805	Streptococcus poly

Putative glycosylt Cpsll protein whic S.thermophilus exo S.thermophilus exo Enzyme EPS5 involv Amino acid sequeon Enzyme EPS7 which	Amino acid sequenc Staphylococcus epi Enzyme EPSB which Amino acid sequenc CpsIK protein whic Streptococcus pneu	Procedured by pr	. 	Campylobacter jeju Campylobacter jeju Streptococcus pneu EpsM. Lactococcus Campylobacter jeju EpsN. Lactococcus Campylobacter jeju Lactococcus lactis
2 AAB96313 1 AAY68974 AAW14078 8 AAW2177 1 AAY54079 1 AAY54071		AAY6896 AAY6896 AAY5408 AAY4378 AAX4378		21 AAY97203 21 AAY97206 22 AAB4720 22 AAB47427 22 AAB47426 21 AAY97213 23 AAB53510
822288	225 227 116 74 84	3 3 3 3 3 3 4 5 4 5 4 5 4 5 4 5 6 6 6 6 6 6 6 6 6 6	37 37 37 37 37	270 301 328 329 3389 2332 302 24
444444 9.8677.52.52		* # # # # # # # # * # # # # # # # # # * # # # #	444444	44444444 110000000
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11 12 13 14 15 17	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	3 5 8 7 6 5 t	33 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	86644444 860112645

ALIGNMENTS

ronic acid; ulcer; nt; bloadhesive.

Pasteurella multocida.

WO200027437-A2

99WO-US26501. 10-NOV-1999; 18-MAY-2000

98US-0107929. 99US-0283402. (OKLA) UNIV OKLAHOMA STATE. 11-NOV-1998; 01-APR-1999;

DeAngelis PL;

WPI; 2000-376319/32. N-PSDB; AAA27449.

Novel method for the enzymatic transfer of sugar molecules to an acceptor, useful for synthesis of e.g. polysaccharide bioadhesives or

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The present sequence is the Pasteurella multocida chondroitan synthase pmCS. PmCS catalyses glycosaminoglycan polymerisation to produce chondroitan: a linear polyaeccharide which has viscoelastic properties which makes it useful for a number of applications. Chondroitan can be used with hyaluronic acid (HA) to coat medical devices e.g. catheters and sensors to reduce tissue abrasion. In addition, they can be used as bloadhesives for haemostatic scaling and healing of wounds and surgical incisions; and as blomaterials that provide sustained delivery of encapsulated drugs, to wounds, ulcers, injuries or surgical sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKLNNIIEYNKNIEVIILHVDKNHLTPDIKKEILAFYHKHQVNILLNNDISYYTSNRLIK 780
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  molecules
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 965; Conservative 0; Mismatches
delivery systems, including hybrid
                         86pp; English.
                          Claim 15; Page 85;
                                                                                                                                                                          965 AA;
                                                                                                                                                                            Sequence
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The present invention relates to the coding sequence of the Pasteurella multocida chondroitin synthase. A chondroitin polysaccharide may be used as a hyaluronan polysaccharide substitute in medial or cometic applications, for example in eye or joint applications, for moisturiser or wound dressings. The enzyme may be used in covalently coupling specific drugs, proteins or toxins to the structurally modified chondroitin for general or targeted drug delivery or radiological procedures, covalently cross linking the hyaluronic acid itself or to other supports to achieve a gel or other three diamensional biomaterial to a surface to create a biocompatible film or monolayer. The present sequence is one version of the protein of the invention.
                                                                                                                                                                                                                                                                                                                                                      Chondroitin synthase; dermatan sulphate; chondroitin sulphate polymer; eye application; joint application; moisturiser; drug delivery; wound dressing; biocompatible film.
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The present invention relates to the coding sequence of the Pasteurella multocida chondroitin synthase. A chondroitin polysaccharide may be used as a hyaluronan polysaccharide substitute in medial or cosmetic applications, for example in eye or joint applications, for moisturiser or wound dressings. The enzyme may be used in covalently coupling specific drugs, proteins or toxins to the structurally modified chondroitin for general or targeted drug delivery or radiological procedures, covalently cross linking the hyaluronic acid itself or to other supports to achieve a gel or other three dimensional biomaterial with stronger physical properties, and covalently linking hyaluronic acid to a surface to create a biocompatible film or monolayer. The present sequence is one version of the protein of the invention.
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This present sequence represents the hyaluronate synthase (pmHAS)

of Pasteurella multocida Carter Type A. The pmHAS enzyme has

different kinetic optima with respect to pH and metal ion

capendence, and different Km values compared with the HAS enzymes

of Streptococcus equisimilis (see AAY06206) and Streptococcus

cyogenes. Km values are about 2- to 3-fold lower for UDP sugars,

cyogenes. Km values are about 2- to 3-fold lower for UDP sugars,

cyogenes are about 2- to 3-fold invertion

cyogenes. Compaining hyaluronate synthase DNA,

cepecially S. equisimilis hyaluronate synthase DNA,

cepecially S. equisimilis hyaluronate synthase DNA,

cand prokaryotic or eukaryotic host cells which produce the enzyme

and its hyaluronic acid product, particularly a product with

modified structure or molecular size. The hyaluronic acid produced

this way is purer than that produced by conventional methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            594 TDGFNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVN 653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNQKTNYPFEVVVADDGSKENLLTIVQKYEQKLDIKYVRQKDYGYQLCAVRNLGLRTAKY 233
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                                                                                                        Nucleic acid encoding hyaluronate synthase for production of hyaluronic acid with controlled molecular weight and targeting specificity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.2%; Score 4486.5;
86.6%; Pred. No. 0;
:ive 63; Mismatches
                                                                                                                                                                                                         Page 123-125; 125pp; English.
Weigel PH
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42; Conservative
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  Kumari
                                                WPI; 1999-337486/28
  DeAngelis P,
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Matches 842;
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This is the Pasturella multocida hyaluronate synthase (PmHAS) amino acid sequence. Hyaluronic acid (HA) or hyaluronan, is a polysaccharide that serves both structural and recognition roles in higher animals. Bacteria produce extracellular capsules of HA which mimic their host HA and aid escape from a host immune response. The invention includes a vector containing the PmHAS nucleotide sequence which can be used to express PmHAS in a foreign host. The HS nucleic acids can be used for the
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TSNRLIKTEAHLSNINKLSQLNLNCEYIIFDNHDSLFVKNDSYAYMKKYDVGMNFSALTH
                                                                                                                                                                                   DWIEKINAHPPFKKLIKTYFNDNDLRSMNVKGASQCMFMKYALPHELLTIIKEVITSCQS
                                                                                                                                                                                                                                  IDSVPEYNTEDIWFQFALLILEKKTGHVFNKTSTLTYMPWERKLQWTNEQIQSAKKGENI
                                                                                                 QSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQNKDAKIAVSIFYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uronate synthase; PmHAS; hyaluronan; hyaluronic acid; HA; delivery; angiogenesis; wound healing; capsule synthesis; cholera; shipping fever.
                                                                                                                                                                                                                                                                                                                                                                                                                                              P. multocida hyaluronate synthase (PmHAS) amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated hyaluronate synthase nucleic acids, used for the production of hyaluronic acid, for developing antibiotics and and for diagnostic applications
                                                                                                                                                                                                                                                                                                                                                                      AAY43099 standard; Protein; 972 AA.
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N-PSDB; AAZ35589.
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production of HA. Also, specific changes to the HS coding sequence can result in the production of HA having a modified size distribution or structural configuration and functional properties. The HA products can be used in e.g. drug delivery, angiogenesis and wound healing, stabilisation of recombinant proteins and in cosmetics. The HS nucleic pacific can also be used to develop agents to block capsule synthesis by pathogens and act as antibiotics. The avirulent P. multocida strains can be used as vaccines for fowl cholera or shipping fever.
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                                                                                                                                   Length 972;
                                                                                                                                                           Indels
                                                                                                                                    DB 21;
                                                                                                                                                         60;
                                                                                                                                  score 4486.5;
Pred. No. 0;
63; Mismatches
                                                                                                                                   88.2%;
86.6%;
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Matches 842; Conservative
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                                                                                                                                                                                Antibacterial; gene therapy; vaccine; blosynthesis; blodegradation; vitamin B12; bacterial infection; disease.
                            MNTLSQAIKAYNSNDYELALKLFEKSAETYGRKIVEFQIIKCKEKL----STNS---YVS 53
                                              LKEFLKDKTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHL
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58;
 58; Mismatches
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     579; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel method for the enzymatic transfer of sugar molecules to an acceptor, useful for synthesis of e.g. polysaccharide bioadhesives or drug delivery systems, including hybrid molecules
            DWIEKTNAHPPFKKLIKTYFNDNDLKSMNVKGASQGMFMTYALAHELLTIIKEVITSCQS
                                                            901 IDSVPEYNTEDIWFQPALLILEKKTGHVFNKTSTLTYMPWERKLQWTNEQTESAKRGENI
                                            894 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKTSTLTYMPWERKLQWTNEQIQSAKKGENI
                                                                                                                                                                                                                                                                                                                                                                     HAS-D; enzyme; ophthalmic surgery; tissue abrasion; bioadhesive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 702;
                                                                                                                                                                                                                                                                                                                                                                     Hyaluronic acid synthase-D; HAS-D; enzyme; ophthalmik
cataract; arthritis; ulcer; tissue abrasion; bloadhek
viscoelastic replacement; hyaluronic acid production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 3079; DB 21;
Pred. No. 1.2e-227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "encoded by AACTGT"
                                                                                                                                                                                                                                                                                                                                       multocida hyaluronic acid synthase-D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
Misc-difference 450
                                                                                                                                                                                                                                    AAY96212 standard; Protein; 702 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 83; 86pp; English
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82.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US26501
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99US-0283402
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                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pasteurella multocida
                                                                                                                                         PVNKFIINSITL 972
                                                                                                                    PVNKFIINSITL 965
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N-PSDB; AAA27448.
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DeAngelis PL;

Sequence Query Match

11-NOV-1998; 01-APR-1999; 10-NOV-1999;

18-MAY-2000

17-AUG-2000

AAY96212;

RESULT AAY9621

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(first entry)

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Enterococcus faecalis cellular proliferation protein #90.
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                  AAU33454;
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monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of

the are useful for selecting probes and primers for detecting genes in L.

monocytogenes and related organisms, and for studying genetic

polymorphisms and other genomes. The present sequence is a protein

encoded by the genome sequence of the present invention. Proteins

cypressed from the genome sequence are useful for raising specific

antibodies, identification of L. monocytogenes and related organisms, and

for blosynthesis and blodegradation, especially blosynthesis of Vitamin

ELS. The genome sequence and proteins encoded by it are also useful for

selecting compounds that regulate gene expression and cell replication

and modulate L. monocytogenes related diseases. In addition, the genome

sequence and proteins encoded by it are useful in pharmaceutical and

vaccines compositions for the treatment or prevention of infections by L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          monocytogenes and related organisms.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                          Cossart P;
                                                                                                                                                                                                                                                                         Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides
                                                                                                                 , Amend A;
Durant L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 FEKENGGGATARNEGLDVATGDYIVMVDSDDYISKNLVETCL-DTVQKTNADLVLFTSYN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRI 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 MSKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDKTLACVYTTNRN 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------LIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGF--- 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -NENIENAVDY - - - DMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKN 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               648 HFVVVNDSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDL---KLIQNKDA 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                         Dehoux P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 PLVSVIIPVYNVEKYVKRCLDSVLEQTYHNLEVIVVNDGATDNSAKVIKSISDN--RIRY 60
                                                                                                                                                                          Hauf J;
                                                 C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; ernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A T, Domann E, Haln T, Berche P, Charbit A, Durant L; J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----YEESKDQLAYLYIEHLIYRLVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.7%; Score 292.5; DB 23; Length 27.5%; Pred. No. 5.5e-14; Live 44; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                       Claim 6; SEQ ID No 1270; 192pp; French.
                                                                        Dussury.
Daniels J, Goere.
Dominguez-Bernal G, Garriuu
Chakraborty T, Domann E, H
Perez-Diaz J, Baquero F, C
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                (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                  WPI; 2002-010914/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           327 AA;
                                                       Buchrieser C,
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AAU33454 standard; Protein; 706 AA

AAU33454 ID AAU RESULT 8

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are scherichia coli, Staphylococcus aucueus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The communiate, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen corrections on the used to screen compounds in rational drug discovery programmes uncleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

On the printed specification, but was obtained in electronic format directly from WIPO at the printed probablished_pct_sequences.
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Best Local Similarity 21.5%; Pred. No. 3.1e-12;
datches 151; Conservative 115; Mismatches 268; Indels 167;
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Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
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                                                                                                                                                                                                                                                                                                                                                              20000S-20648P.
20000S-207727P.
20000S-242578P.
20000S-255625P.
20000S-257931P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ELIT-) ELITRA PHARM INC.
                                                                                               Enterococcus faecalis.
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22-DEC-2000;
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Query Match
Best Local Similarity
Matches 151; Conserv
Xu HH;
               2001-611495/70.
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                        N-PSDB; AAS52777
Yamamoto RT,
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                                                                                                            280 FYEVVKVLNENPELDLIXSDEDKIDMDGNRSDPAFK-PDWSPDLLLGTNYISHLGVYRRS 338
                                                                                                                                  644
                   161
                                                                                                                                                                                                                                           488 AKFEQOLPGREFVESIDIPF------NESTINNRAAKKAHGEYLLELNNDTEVIT
                                                                                                                                              645 KKNHFVVVNQSLNRQGINYYN----YDKFDDLDESRKYIFNKTAEYQEEMDMLKDL
                                                                                                                                                                                                  KLIQNKDAKIAVSIFYPNTLNG---LVKKKLNNIIEYNKNIFVIILHVDKNHLTPDIKKEI
                                                                                                                                                                                                                                 754 LAFYHKHQVNILLNN-DISYYTSNRLIKTEAHLSNINKLSQLNLNCEYIIFDNHDSLFVK
                                                                                                  530 VELCLKEFLKDKTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIR
                                                                                                                                  590 AWHLTDGFNENIENAVDYDMFLKLSE---VGKFKHLNKICYNRVLHGDNTSIKK--LGIQ
                                                                                                                                                                             DEEFNHWGGEDVEFGYRLFAKGCFFRVIDGGMAIHQEPPGKENETEREAGKSITLKIVKE
                   -----IKAKKGFKYMAKNGIS-HTIQRAKIEKLRNQA--SYLNWLARN
                                  KVPYIYRKLLPIEDSHIHRIPLVSIYIPAYNC-ANYIQRCVDSALNQTVVDLEVCICNDG
                                             472 STD-NTLEVINKLYGNNPRVRIM-SKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                        Enterococcus faecalis cellular proliferation protein #205.
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2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-25931P.
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27-NOV-2000;
22-DEC-2000;
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26-MAY-2000;
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                      DKVTRLW-
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The invention relates to antisense inhibitors of genes essential to prokaryotic callular proliferation, their use in identifying the genes, their use in the discovery of novel antiborities, the essential comes, their use in the discovery of novel antiborities, the essential comes, their use in the discovery of novel antiborities, the essential comes are themselves and the encoded proteins. The proteins coll, Staphylococcus aud Enterococcus facelis: The neumoniae, Pseudomonas acrudinosa and Enterococcus facelis: The cinvention is also useful for the identification of potential new targets for antibotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery corporammes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic callular proliferation protein.

Control of the printed specification, but was obtained in electronic form and directly from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    341 ILEEIGGFRKGYEGSQDYDLVLRFTEKTTKERITHIPKVLYYWRMLPTSTAVDQGSKGYA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLIQNKDAKIAVSIFYPNTLNG---LVKKLNNIIEYNKNIFVIILHVDKNHLTPDIKKEI 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKVTRLW------IKAKKGFKYMAKNGIS-HTIQRAKIEKIRNQA--SYLNWIARN 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :| | : : | : | : | : | : | : | | : | | | EVLDI - - EAMTQEIATFHYQPKISIAMPVYNVEEKWLRLCIGSILNQVYTNWELCMADDA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 DNDIVLIGPRKYVD--THNITAEQFLNDPYLIESLPETATNNNPSITSKGNISLDWR--- 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FYEVVKVLNENPELDLIYSDEDKIDMDGNRSDPAFK-PDWSPDLLLGTNYISHLGVYRRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEEFNHWGGEDVEFGYRLFAKGCFFRVIDGGMAIHQEPPGKENETEREAGKSITLKIVKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- LEHEKKTDNLRLCDSPFRYFVAGNVAFSKEWLNK----VGWF
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11.5%; Pred. No. 3.2e-12;
ve 115; Mismatches 268; Indels 167;
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New polynucleotides for the identification and development antiblotics, comprise sequences of antisense nucleic acids
                                                                                                        English.
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                                                                                                        Example 3; Seq ID No 10511; 511pp;
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Length 321;

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Similarity
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 Query Match
Best Local S
Matches 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus progenese (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to detect Streptococcus in a biological sample. (I) are used to detect of encoding (I), may be used to detect of encoding (I), may be used to recombinantly produce (I) and may be used in gene therapy. Antiboddes to (I) are used for affinity chromogoraphy. Immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                             Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
539 ENWLTLMVSFAQQERIGCVGAKLLYPNNTVQHAGVILGLGGVAGHGHYGYPHGDLGYFGR 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grandi G,
                                                                                                   822 YDVGMNFSALTHDWI----EKINAHPPFKKLIKTYFNDNDL 858
                                                                                                                      Masignani V, Margarit Ros YI,
                                                                                                                                                                                                                                                                                                  Streptococcus polypeptide SEQ ID NO 2786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 3429; 4525pp; English.
                                                                                                                                                                                                           ABP26805 standard; Protein; 321 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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                                                                                                                                                                                                                                                                      (first entry)
              490 AKFEQQLPGRFFVESIDIPF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus proteins.
                                           ND----SYA----
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N-PSDB; ABN67436.
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Tettelin H;
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                                                                                                                                                                                                                                                                                                                                                                                           R----NVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGFNENIENAV 605
                                                                                                                                                                                                                                                       123 REQHIINIVLEDEMI------ETISPV-----------QAIQNIY 150
                                                                        435 VSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIMS 494
                                                                                                                                               495 KPNGGIASASNAAVSFAKGYYIGQLDSDDYL-EPDAVELCL---KEFLKDKTLACVYTTN 550
                                                                                                                                                                                                                                                                                                                                                                      666 YDKFDDLDESRKYIFNK----TAEYQEEMDMLKDLKLIQNKDAKIAVSIFYPNTL----N 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 ALIKTMEVNLIELYKNNFYKEFHT----LKTEYKKTIFDFIKKQRMLLKIKYYLKYCVVH 307
                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative glycosyltransferase, involved in cell wall biogenesis #1.
                                                                                                                                                                                                                                                                                             DYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVNQSLNRQGINYYN
                                                                                                                                                                                                                                                                                                                                                                                                                                             718 GLVKKLN-NIIEYNKNIFVIILHVDKNHLTPDIKKEILAFYHKHQVNILLNNDISYYTSN
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                                      74;
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                                      Indels
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5.0%; Score 253; DB 23;
25.1%; Pred. No. 5.8e-11;
iive 64; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Pages 981-982; 1657pp; French.
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(IFRE-) IFREMER INST FR RECH EXPL MER.
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mutants for vaccination
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                                                                                                                                                                                                                                999
                                                                                                                                                                                                                                                                                                                    Capsular gene cluster; serotype 1; polysaccharide biosynthesis; capsular component; antigen; regulation; chain length determination; complement-mediated opsonophagocytosis; serotype-specific detection; antigen; vaccine; Streptococcal disease; CpslE; CpslE; CpslG; CpslH; CpslJ; CpslK; glycosyltransferase; CP polymerase.
                                                                                                                                                                        492 IMSKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLK-DKTLACVYTTN 550
                                                                                                                                433 PLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVR- 491
                                                                                                                                             uses, since the proteins are stable at very high temperatures, some ulso degrees centigrade.

Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG66436.
                                                                                                             Gaps
                                                                                                                                                                                                                   RNVNPDGSLIANGYNWPEFSREKLTTAMIAHHF-----RWFTIRAWHLTDGFNENIENAV
                                                                                                                                                                                        62 IRLKKNSGSPIARNIGIKKAKGRFIALLDDDDEWLPHRLEVQVRKFENLGKEFCVVYGGF
                                                                                                                                                                                                                                                            DYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVNQSLNRQGINYYN
                                                                                                                                                                                                                                                                                                     YDKFDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQNKDAKIAVSIFYPNTLNGLVKKLN-
                                                                                                             50;
  proteins are stable at very high temperatures,
                                                                                       Length 298;
                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cps11 protein which has glycosyltransferase activity.
                                                                                                                                                                                                                                                                                 DWDMWLRIARYYKFDYVDEIIAKYYVHGKQISF------
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                                                                                       Query Match
4.9%; Score 251; DB 22;
Best Local Similarity 24.3%; Pred. No. 7.3e-11;
Matches 81; Conservative 66; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                 --NIIEYNKNIFVIILHVDKNHLTPDIKKEILA 755
                                                                                                                                                                                                                                                                                                                                                            264 SIAIAPLNLENYMILLKLALDSRTVEYIKRILS 296
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                                                                      298 AA;
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22-JUL-1998;
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                                                                      Sequence
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15;
                                                                                                                      Streptococcus such serotype 1. The genes in this cluster are involved in polysaccharide biosynthesis of capsular components and antigens. The proteins have glycosyltransferase activities (CpslE, CpslG, CpslI, Cps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -FVVVNQSLNRQGINYXNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQNKDAKIA 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       434 LVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIM 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NPDGSLIA-----NGY----NWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGF 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 LISVIVPLIYNVQDYLDKCINSIINQTYTNLEVILVNDGSTDDSEKICLNYMKNDGRIKYY 63
                                                                                           proteins AAY68970-76 are encoded by the capsular gene cluster of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           operon; lactic acid bacterium; epsF; epsG; epsH; epsI; epsJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 GSNIEN----NVWCKLYSRDIIKDIKFQINNRSIGEDLLFNLEVLNNVTRVVVDTREYYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 SKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDKTLACVYTTNRNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.8%; Score 246; DB 21; Length 322;
25.3%; Pred. No. 2e-10;
tive 58; Mismatches 120; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S.thermophilus exopolysaccharide biosynthesis enzyme EpsH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus thermophilus strain Sfi6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Exopolysaccharide biosynthesis; epsepsR; epsA; epsB; epsC; epsD; epsE; epsK; epsL; epsL; cNCM I-1590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW14078 standard; Protein; 324 AA
Disclosure; Fig 4; 144pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  763 NILL 766
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This sequence represents the protein encoded by the epsI gene from the Streptococcus thermophilus exopolysaccharide (EPS) synthesis operon. The operon has 13 open reading frames (ORF) designated epsA-M encoding proteins AAW22169-81. This protein has 24% identity to a protein encoded by the RfbV ORF of the rfb cluster from Salmonella typhimurium and is probably a glycosyl transferase. The EPS are useful for thickening e.g. drinks, liquid desserts, yoghurts, soups, ice-creams, coffee creams, sauces, mayonnaise.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    722 KLNNIIEYNKN-IFV----IILHVDKNHLTPDIKKEILAFYHKHQVNILLNNDISYYTSN 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 OFPNLALYVKNRAFAAEVKIFLEIPKEKEFEQAQKQL----WH-----DIKKNRKAPFMTKG 295
 Streptococcus thermophilus; operon; exopolysaccharide; synthesis; open reading frame; thickening; drink; liquid dessert; yoghurt; soup; sauce; ice-cream; coffee cream; mayonnaise; glycosyl transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 434 LVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIM 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         662 NYYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQNKDAKIAVSIFYPNTLNGLVK 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 LISIVIPVYNVEKYLEKCLQSVQNQTYNNFEVILVNDGSTDSSLSICEKFVNQDKRFSVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 DAYDYAYVQRPNSIMNSSFN------LKKLDIIE-------MVHEMENDILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      602 ENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVNQSLNRQGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 ONGYDLAVWGKLYPVSFFETIS-FPEGKLYEDMGTTYKLLKLASEVVF-----L
                                                                                                                                                                                                                                                                                                                                                          - encoding enzymes involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -------KGSLLTK----KEAPKKKSEVVSIEESIKILLLO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.7%; Score 238.5; DB 18;
23.9%; Pred. No. 7.6e-10;
Live 58; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVE-----
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                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 14-28; 46pp; French
                                                                                                                                                                                                                                                                                                                                                        DNA of lactic acid bacteria – er
exo-polysaccharide biosynthesis
                                                                                                                                                                                                     95EP-0201669.
                                                                  Streptococcus thermophilus
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                                                                                                                                                                                                                                        (NEST ) SOC PROD NESTLE
                                                                                                                                                                                                                                                                       Mollet B, Stingele F;
                                                                                                                                                                                                                                                                                                         WPI; 1997-044837/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324 AA;
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                                                                                                                                                                                                     20-JUN-1995;
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                                                                                                                                   27-DEC-1996
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AAY54079
ID AAY54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : |:| :: | :: | DAYDYAVQRPNSIMNSSFN------LKKLDIIE--------WYHEMENDIILA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLNNIIEYNKN-IFV----IILHVDKNHLTPDIKKEILAFYHKHQVNILLNNDISYYTSN 776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIM 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 LISIVIPVINVEKYLEKCLQSVQNQTYNNFEVILVNDGSTDSSLSICEKFVNQDRRFSVF 65
                                                                                                                                                                                                                                               A chromosomal DNA sequence representing practically the whole eps (exopolysaccharide blosynthesis) operon from Streptococcus thermophilus strain Sife (deposited as CNCM 1-1590) was isolated. The sequence contained 14 open reading frames, one of which was located on the complementary strand. The present sequence is decoded from the epsH open reading frame. The EpsH protein is probably a glycosyl transferase.

Novel exopolysaccharides can be produced by transforming lactic acid bacteria which produce exopolysaccharides with DNA encoding at least one enzyme from the eps operon. The new exopolysaccharides are useful for thickening drinks, liquid desserts, yoghurts, soups, ice-creams, coffee creams, sauces, mayonnaise, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S.thermophilus exopolysaccharide synthesis operon epsI gene product.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 18; Length 324;
                                                                                                                                                                     - encoding enzymes involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.7%; Score 238.5; DB 18;
23.9%; Pred. No. 7.6e-10;
Live 58; Mismatches 139;
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                                                                                                                                                                                                                   Claim 7; Pages 33-34; 42pp; French
                                                                                                                                                                                   exo-polysaccharide biosynthesis
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                 95EP-0201669
                                                   SA.
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ARLKNRLGASLSFLGK 311
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                                                 (NEST ) SOC PROD NESTLE
                                                                               Stingele F;
                                                                                                                WPI; 1997-044836/05
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                                                                                                                                   N-PSDB; AAT62328
               20-JUN-1995;
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                                                                                Mollet B,
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661

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Exopolysaccharide, EPS; ESP enzyme; EPS1; EPS2; EPS3; EPS4; EPS5; EPS7 EPS7; EPS7; EPS8; EPS9; EPS10; EPS11; Lactobacillus helveticus strain LH59; activated D-galactose pyranose; saccharide; beta-glycosyltransferase; undecaprenyl-hosphate-glycosyl-1-phosphate-transferase; alpha-glycosyltransferase; EPS polymerase; glycosyltransferase; phosphofuranose; transporter; food; fermented milk product; yoghurt; cheese; flavour stability; organoleptic property.
                                                                                                                                                                                                                                                                                                                                                  New recombinant enzymes for synthesis of exopolysaccharides, particularly in lactic acid bacteria, for improving properties of fermented milk products
                                                                                                                                                                                                                                                                                                                               N-PSDB; AAZ45259, AAY54082, AAY54083, AAY54084; AAX54085.
                                            Enzyme EPS5 involved in exopolysaccharide biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page 122-123; 162pp; French.
                                                                                                                                                                                                                                    98EP-0201310.
98EP-0201311.
98EP-0201312.
                                                                                                                                                                                                                  99WO-EP02841
                                                                                                                                                                                                                                                                               (NEST ) SOC PROD NESTLE SA
                           (first entry)
                                                                                                                                                                                                                                                                                                    Germond JE,
                                                                                                                                                     Lactobacillus helveticus
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22-APR-1998;
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                            27-MAR-2000
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        AAY 54079;
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Lamothe G;

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AAYSAU,J-10. Tepresent enzymes involved in the Dissylthebile.

Exopolysaccharides (EPS). These enzymes are designated EPSI-EPSI. and are encoded by open reading frames epsi-epsil. The enzymes are isolated from Lactobacillus helveticus strain LHS9. The proteins are used in method for the synthesis of EPS, which includes at least one step of forming a bond (alpha or beta-isomer) between C-1 (carrying the of forming aldehyde function, of an activated D-galactose pyranose), and a phosphate on a lipophilic or proteinaceous primer. Stepwise synthesis of EPS occurs with, in each step, addition of a new sugar unit, through the hemit, present at the end of a chain of sugar residues bonded to the unit, present at the end of a chain of sugar residues bonded to the prophate-transferase; EPS2, EPS3 and EPS4 are alphating phosphate-transferase; EPS5 and EPS6 have homology with an beta-phosphate-transferase; EPS5 and EPS6 have homology with a beta-phosphate-transferase; EPS5 and EPS6 have homology with a beta-phosphate-glowing repetitive unit; EPS10 transfer of phosphoturanose is a glycosyltransferase; EPS9 calalyses the transfer of phosphoturanose is a glycosyltransferase; EPS9 exalyses the transfer of phosphoturanose of force the following repetitive unit; EPS10 transports the polysaccharides conto the EPS enzyme are used to improve properties of formed particularly fermented milk products such as yoghurt and cheese, e.g. their organoleptic properties and flavour stability.
AAY54075-85 represent enzymes involved in the biosynthesis of
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DB 21; Length 339;
4.5%; Score 230.5; DB 21;
25.2%; Pred. No. 3.4e-09;
tive 64; Mismatches 131;
                Local Similarity
hes 93; Conserv
         Query Match
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Indels

PLVSIYIPAYNCANYIQRCVDSALNQTVVD-LEVCICNDGSTDNTLEVINKLYGNNPRVR 491

Conservative

Best Loca Matches 433

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492 IMSKPNGGIASASNAAVSFAKGYYIGQLDSDDYLE------PDA--VELCLKEFL 538

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699 IQN-KDAKIAVSIFYPNTLNGLVKKLNNIIEYNKNIFVIILHVDKNHLTPDIKKEILA-- 755
                                                                                                                                                                                                                                                                              279 INNDKNKKLQKEVYWQ-----AYKLKRYVFKSKSI-------PVSKKMFFACT 319
                                                                            123 KLNTNNKLLEBYKFSNVTRSAEDVISLLLNETGPQGYLWNKMFR----TSIIKKYSLLLD 178
K----DKTLACVYTTN--RNVNPDGSLIAN-----GYNWPEFSREKLTTAMIAHHFRMFT
                                                                                                                                             179 PKIF-----MAEDLLECIQYLKFSKKVRVSNYCDYNYVQDSNSMNGGLSFTKNNRRYKKI
                                                                                                                                                                                642 GIQKKNHFVVVNQSLNRQGINYNYDKFDDLDESRKY---IFNKTAEYQEEMDMLKDLKL
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EPS3; EPS4; EPS5; EPS6;

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January 4, 2003, 02:22:39 ; Search time 66 Seconds (without alignments) 430.199 Million cell updates/sec
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1 MNTLSQAIKAYNSNDYELAL.....SAKKGENIPVNKFIINSITL
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                              OM protein - protein search, using sw model
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Perfect score:
Sequence:
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Issued_Patents_AA:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	ocuantos sedneuce sedneu
SUMMARIES	US-09-437-277-3 US-09-437-277-3 US-08-137-277-1 US-08-134-001C-4067 US-08-134-001C-4067 US-08-131-3878-10 US-08-131-3878-11 US-08-131-3878-13 US-08-683-426-13 US-08-683-426-13 US-08-683-426-13 US-08-683-428-11 US-08-683-428-11 US-08-9733-412-11 US-08-9733-412-13 US-09-333-412-13 US-09-333-412-13 US-09-333-412-13 US-09-333-412-13 US-09-333-42-12 US-08-683-426-5 US-08-683-426-5 US-08-683-426-5 US-08-683-428-5 US-08-683-428-12 US-08-683-428-5 US-08-683-428-12 US-08-683-428-12 US-08-683-428-12 US-08-683-428-12 US-08-683-428-12 US-08-683-428-12
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87	503	4 . 1	337	7	US-08-878-360-12	Sequence 12, Appl
29	209	4.1	337	m	US-08-478-140B-5	Sequence 5, Appl1
30	209	4.1	337	4	US-09-333-412-5	Sequence 5, Appl1
31	209	4.1	337	4	US-09-333-412-12	Sequence 12, Appl
32	209	4.1	337	4	US-09-338-943-5	2, 2
33	178.5	3.5	990	~	US-08-392-625-20	Sequence 20, Appl
34	178.5	3.5	066	~	US-08-466-961A-20	20,
35	176.5	3.5	066	~	US-08-645-193B-15	15,
36	174.5	3.4	2710	Н	US-08-480-604A-6	Sequence 6, Appl1
37	174.5	3.4	2710	~	US-08-405-496A-6	9
38	174.5	3.4	2710	4	US-08-915-136-6	9
39	174.5	3.4	2710	4	US-08-957-310-6	Sequence 6, Appl1
40	173.5	3.4	281	4	US-08-961-083-196	19
41	167.5	3.3	270	4	US-08-961-083-198	198,
42	156.5	3.1	633	~	US-08-648-298-2	Sequence 2, Appli
43	156.5	3.1	10182	4	US-09-134-001C-3159	
44	156	3.1	418	4	US-09-134-001C-4051	4051,
45	153.5	3.0	926	4	US-09-134-001C-4452	
					ALIGNMENTS	
RESULT 1 US-09-437-277-3	7-277-3					

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KDFPKDLVLAPLPDHVNDFTWYKKRKKRLGIKPEHQHVGLSIIVTTFNRPAILSITLACL 180
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Fatent No. 5733765
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: STINGELE, Franscesca
APPLICANT: MOLLET, Beat
TITLE OF INVENTION: LACTIC BACTERIA PRODU
TITLE OF INVENTION: LACTIC BACTERIA PRODU
TITLE OF INVENTION: LACTIC BACTERIA PRODU
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americans
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95201669.9
FILING DATE: 20-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/597, 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/597,236
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Fanucci A., Allan
REGISTRATION NUMBER: 30256
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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          601 IENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVNQSLNRQG
                                                                          541 KTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGFNEN
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Sequence 1, Application US/09437277

Sequence 1, Application US/09437277

Sequence 1, Application US/09437277

Sequence 1, Application US/09437277

GENERAL INFORMATION:

APPLICANT: THE BOARD OF RECENTS OF THE UNIVERSITY OF OKLAHOMA APPLICANT: S000.531

CURRENT PAPLICATION NUMBER: US/09/437,277

CURRENT APPLICATION NUMBER: US/09/437,277

CURRENT PILING DATE: 1999-11-10

NUMBER OF SEO ID NOS: 6

SOFTWARE: WordPerfect 8.0 (saved in ASCII format)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8,
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Best Local Similarity 82.4%; Pred. No. 1.1e-260;
Matches 579; Conservative 58; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Pasteurella multocida
US-09-437-277-1
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|| NSITL 965
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LENGTH: 702
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                                         ETATINNPSITSKGNISLDWRLEHFKKTDNLRLCDSPFRYFVAGNVAFSKEWLNKVGWFD
                                                                                               EEFNHWGGEDVEFGYRLFAKGCFFRVIDGGMAIHQEPPGKENETEREAGKSITLKIVKEK
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           VNOKTNYPFEVVVADDGSKENLLTIVQKYGQKLDIKYVRQKDYGYQLCAVRNLGLRTAKY
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GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCOCC
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1990-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
RICH APPLICATION NUMBER: US 60/065,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---- MVHEMENDILA 242
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                                                                                                                                                                                                                                                                                                                                                                    -----KEAPKKKSEVVSIEESIKILLLQ-----KGSLTKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 QNGYDLAVWGKLYPVSFFETIS-FPEGKLYEDMGTTYKLLKLASEVVF-----L 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             722 KLNNIIEYNKN-IFV----IILHVDKNHLTPDIKKEILAFYHKHQVNILLNNDISYYTSN 776
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                                                                                                                                                                                                                                                         434 LVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIM 493
                                                                                                                                                                                                                                                                                                                                              494 SKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVE------LCLKEFLKDK 541
                                                                                                                                                                                                                                                                                                                                                                                                                                     542 TLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGFNENI 601
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22.8%; Pred. No. 4.4e-11;
tive 66; Mismatches 161; Indels 192;
                                                                                                                                                                         Length 324;
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    INFORMATION FOR SEQ ID NO: 10:
                                            : 324 amino acids amino acids
                                                                                                                                                                                           Best Local Similarity 23.9%
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               777 RLIKTE--AHLSNINK 790
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296 ARLKNRLGASLSFLGK 311
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                        SEQUENCE CHARACTERISTICS
                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-746-682A-10
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Best Local Similarity
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US-09-134-001C-4067
                                        LENGTH:
                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                    494 SKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVE------LCLKEFLKDK 541
                                                                                                                                                                                                                                                                                                                                                                                        542 TLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRWFTIRAWHLTDGFNENI 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         602 ENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVNQSLNRQGI 661
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                                                                                                                                                                                                               434 LVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIM 493
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                     -------KGSLLTK----KEAPKKKSEVVSIEESIKILLLQ------
                                                                                                                               Length 324;
                                                                                                                          4.7%; Score 238.5; DB 1; Length: 23.9%; Pred. No. 1.2e-12;
tive 58; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/746,682A
FILING DATE: 14-NOV-1996
RIOR APPLICATION: 435
RIOR PROFITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: STINGELE, Franscesca
APPLICANT: MOLLET, Beat
TITLE OF INVENTION: LACTIC BACTERIA PRODUCING
TITLE OF INVENTION: EXOPOLYSACCHARIDES
CORRESPONDENCE: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/597,236
FILING DATE: 20-UNN-1995
APPLICATION NUMBER: EP 95201669.9
FILING DATE: 20-UNN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-746-682A-10; Sequence 10, Application US/08746682A; Patent no. 5786184; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Fanucci A., Allan REGISTRATION NUMBER: 30256
324 amino acids
amino acid
                                                                                                                      Query Match
Best Local Similarity 23.9%
Matches 90; Conservative
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296 ARLKNRLGASLSFLGK 311
                      ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-597-236-10
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STATE: New York
COUNTRY: U.S.A.
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  LENGTH:
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823 -----DVGMNFSALTHDWIEKINAHPPF---KKLIKTYFND------NDLRSMNVK 864
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                                                                                                                                                                                                                                       204 FNFPFFFRGEVYDPFETLTLS-------EQNFDILFKDY------VNSFYD 241
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69 IDLDENSGHAHARNIALEEVETPYFMFLDADDELASYAITFYLEKFNNTDGLIAPIHSFT-128
                                        TNRNVNPDGSLIANGY----NWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGFNENIEN 603
                                                                                                                 604 AVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVNQSLNRQGINY 663
                                                                                                                                                            -----VRI 203
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Sequence 200, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                   242 AIKRATNPKVREFIVTKMGNKIANEFEPTRYDIN-----ERYOTHKDTLVELSKFLH
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP VECTER 486/33
OPERATING SYSTEM: MSDOS VERSION 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                              795 -NLNCEYIIFDNHDSLFVKNDS-----YAYMKKY----
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                                                                                                                                                 NAME: Brookes, A. Anders
REGIETRATION UNUMBER: 36,373
REPERENCE/DOCKET UNWBER: PB34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPRAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 200:
SEQUENCE CHARACTERISTICS:
LENGTH: 674 amino acids
TYPE: amino acid
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CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----YHKHQVNILLINNDISYYTSNRLIKTEAHLSNINKLSQLNLNCEYIIFDNHDSLFVK 812
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TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
                                                                                                                                                                                 Length 674;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       511 AKGYYIGOLDSDDYLEPDAVELCLK---EFLKDKTLACVYTTNRN--
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/312,387B
                                                                                                                                                                                 Query Match
Best Local Similarity 20.1%; Pred. No. 7.8e-11;
Matches 96; Conservative 89; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: July 7, 1994
CLASSIFICATION: 435
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REGISTRATION NUMBER: 600-1-095
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08312387B Patent No. 554553
GRNEAL INFORMATION:
APPLICANT: Gotschlich, Emil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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                                                                      , MOLECULE TYPE: protein US-08-961-083-200
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Jersey
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
CLASSIFICATION: 535
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-09
TELECOMMUNICATION INPORMATION:
TELECHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08683426 Patent No. 5705367
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411 Hackensack Avenue
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TELEX: 133521
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
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amino acid
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; MOLECULE TYPE: protein US-08-312-387B-11
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: New Jersey
RY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U
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Patent No. 554553
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL GENSENIED, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 QKTARNDFL---QSMGFK-----TRFDSLE----YRQTKAAAYELPEKDL 278
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                                                                                                                                                                                         Length 348;
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26.4%; Pred. No. 4.1e-10;
tive 57; Mismatches 110; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/312,387B
FILING DATE: U1y 7, 1994
CLASSIFICATION: 435
ATTONREY/AGENT INPOMBATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
RECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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411 Hackensack Avenue
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
             TELEX: 133521
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 348 amino acids TYPE: amino acid
                                                                                                                                                                                                                           77; Conservative
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201 343-1684
                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-312-3878-3
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber &
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MEDIUM TYPE: Floppy
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STATE: New Jersey
COUNTRY: USA
ZIP: 07601
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Best Local Similarity
Matches 77; Conserva
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TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                       433 PLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRI 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               493 MSK-PNGGIASASNAAV-SFAK-----GYYIGQLDSDDYLEPDAVELCLKEFLKDKTLAC 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                546 V--YTTNRNVNPDGSLIA----NGYNWPEFSREKLTTAMI-----AHHFRMFTIRAWHLT 594
                                                                                                                                                                                         Gaps
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APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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         Length 348;
Query Match
4.1%; Score 210; DB 1; Length 348
Best Local Similarity 26.4%; Pred. No. 4.1e-10;
Matches 77; Conservative 57; Mismatches 110; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentur Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,426
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                                                                                                                                                                                                     493 MSK-PNGGIASASNAAV-SFAK----GYYIGQLDSDDYLEPDAVELCLKEFLKDKTLAC 545
                                                            433 PLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRI 492
                                Gaps
                                                                           DG---FNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIK------KLGI
                                                                                                                                                                                                                                                                             181 DGGLRYDTERDWAEDYQFWYDVSKLGRLAYYPEALVKYRLHANQVSSKHSVRQHEIAQGI
                                                                                                                                                                                                                                                                                                                                                                                           48;
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4.1%; Score 210; DB 1; Length 348;
Best Local Similarity 26.4%; Pred. No. 4.1e-10;
Matches 77; Conservative 57; Mismatches 110; Indels
4.1%; Score 210; DB 1; Length 348; 26.4%; Pred. No. 4.1e-10; tive 57; Mismatches 110; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
CLASSIFICATION: 536
ATTORNEY, AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
RREFERENCE/COCKET NUMBER: 600-1-095B
TELECOMMUNICATION:
TELECHONE: 201487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/683,426
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
TOPOLOGY: linear
Query Match
Best Local Similarity 26.4%
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 343-1684
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CITY: Hackensack
STATE: New Jersey
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                                                                                                                                                                                                               546 V--YTTNRNVNPDGSLIA----NGYNWPEFSREKLTTAMI----AHHFRMFTIRAWHLT
433 PLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRI
                                                                                                                                                                                                                                                                            595 DG---FNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIK-----KLGI
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Sequence 3, Application US/08683458
Sequence 3, Application US/08683458
Patent No. 579823
GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                     644 QK--KNHFVVVNQSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQ-EEMDM 692
                                                                                                                                                                                                                                                                                                                                                                                                         241 QKTARNDFL---QSMGFK-----TRFDSLE----YRQTKAAAYELPEKDL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 348;
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4.1%; Score 210; DB 1; Length 348
Best Local Similarity 26.4%; Pred. No. 4.1e-10;
Matches 77; Conservative 57; Mismatches 110; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
CLASSIFICATION: 435
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ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REPRENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201,487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 348 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Jersey
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07601
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14; : : | | : | | : : | 180
123 MGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAFFPFGNPIHNNTWIMRRS--VI 180 433 PLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRI 492 Gaps

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V--YTTNRNVNPDGSLIA----NGYNWPEFSREKLTTAMI-----AHHFRMFTIRAWHLT 594
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SACCHARIDE UNITS WITH A POLYGLYCOSYLTRANSFERASE,
POLYGLYCOSYLTRANSFERASE AND GENE ENCODING A
POLYGLYCOSYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       433 PLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRI 492
                                                                                                                      181 DGGLRYDTERDWAEDYQFWYDVSKLGRLAYYPEALVKYRLHANQVSSKHSVRQHEIAQGI 240
                                      123 MGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAFFPFGNPIHNNTMIMRRS--VI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                546 V--YTTNRNVNPDGSLIA----NGYNWPEFSREKLTTAMI-----AHHFRMFTIRAWHLT
                                                                                  DG---FNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIK-----KLGI
                                                                                                                                                                   644 QK---KNHFVVVVNQSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQ-EEMDM 692
                                                                                                                                                                                          241 QKTARNDFL---QSMGFK-----TRFDSLE----YRQTKAAAYELPEKDL 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/478,140B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               core 210; DB 3;
red. No. 4.1e-10;
Mismatches 110,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.1%; Score 210;
26.4%; Pred. No. 4
:ive 57; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08478140B Patent No. 6127153
GENERAL INFORMATION:
APPLICANT: JOHNSON, KARL F.
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: JOHNSON, KARL F.
APPLICANT: ROTH, STEPHEN
APPLICANT: BUCZALA, STEPHANIE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Laura A. Coruzzi
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7188
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (212) 790-9090
(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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N: 435
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Best Local Similarity 26.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-478-140B-3
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US-08-478-140B-3
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                                                                                                                                                            181 DGGLRYDTERDWAEDYQFWYDVSKLGRLAYYPEALVKYRLHANQVSSKHSVRQHEIAQGI 240
63 LAQAQNSGLIPSLNIGLDELAKSGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 122
                                      546 V--YTTNRNVNPDGSLIA----NGYNWPEFSREKLTTAMI-----AHHFRMFTIRAWHLT 594
                                                                                                                    595 DG---FNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIK-----KLGI
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: GOLSCHlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                  644 QK---KNHFVVVVNQSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQ-EEMDM 692
                                                                                                                                                                                                                              241 QKTARNDFL---QSMGFK-----TRFDSLE----YRQTKAAAYELPEKDL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,360
FILING DATE: 18-JUN-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.1%; Score 210; DB 2; L
26.4%; Pred. No. 4.1e-10;
ive 57; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: September 26, 1994
CLASSIFICATION: 435
ATOMNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/POCKET NUMBER: 600-1-09:
TELECOMMUNICATION INFORMATION:
TELECPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/683,426
                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/08878360 Patent No. 5945322 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08/312,387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 133521
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 26.48
Matches 77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-08-878-360-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Hackenser
STATE: New Jersey
COUNTRY: USA
7.IP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Linear
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US-08-878-360-11
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LSEEKDGNRLARHHKHGKI
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595 DGFNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGI 643	_ _
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¹⁸¹ DGGLRYDTERDWAEDYQFWYDVSKLGRLAYYPEALVKYRLHANQVSSKHSVRQHEIAQGI 240

Search completed: January 4, 2003, 02:29:20 Job time : 71 secs

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us-09-842-484a-2.rapb

Page

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GenCore version 5.1.3
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OM protein - protein search, using sw model

January 4, 2003, 02:26:45; Search time 203 Seconds Run on:

(without alignments) 90.090 Million cell updates/sec

Title: Perfect score:

US-09-842-484A-2 5089 1 MNTLSQAIKAYNSNDYELAL......SAKKGENIPVNKFIINSITL 965

Sequence:

Scoring table:

117078 segs, 18951520 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

Published_Applications_AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 10, Appl	Sequence 4950, Ap	Sequence 10511, A		Sequence 22, Appl	Sequence 36, Appl	Sequence 200, App	Sequence 21, Appl	Sequence 3, Appli	Ξ	Sequence 5, Appli	Sequence 12, Appl	Sequence 39, Appl	27,	Sequence 34, Appl		31,		Sequence 35, Appl
	ID	US-09-879-959-10	US-09-815-242-4950	US-09-815-242-10511	US-09-767-041-34	US-09-767-041-22	US-09-767-041-36	US-09-765-272-200	US-09-767-041-21	US-10-007-267-3	US-10-007-267-11	US-10-007-267-5	US-10-007-267-12	US-09-816-028A-39	US-09-816-028A-27	US-09-816-028A-34	US-09-816-028A-29	US-09-816-028A-31	US-09-767-041-52	US-09-767-041-35
	DB	6	10	10	10	10	10	10	10	12	12	12	12		10			10	10	10
	Duery Watch Length DB	972	206	715	322	332	278	674	332	348	348	337	337	270	301	389	303	297	120	322
ф	Ouery Match	88.2	5.4	5.4	4.8	4.4	4.4	4.4	4.3	4.1	4.1	4.1	4.1	4.1	4.1	4.0	3.9	3.9	3.8	3.8
	Score	4486.5	276.5	276.5	246	224	223.5	223.5	217.5	210	210	209	209	208.5	207	202	200.5	199	194	194
	Result No.	-	7	e.	4	5	9	7	80	6	10	11	12	13	14	15	16	17	18	19

Sequence 51, Appl Sequence 296, Appl Sequence 3805, Ap Sequence 196, Appl Sequence 197, Appl Sequence 11, Appl 1 Sequence 11, Appl 1 Sequence 13, Appl Sequence 13, Appl Sequence 5114, Appl Sequence 5114, Appl Sequence 26, Appl 1 Sequence 354, Appl 1 Sequence 354, Appl 1 Sequence 1, Appl 1 Sequence 26, Appl 1 Sequence 27, Appl 1 Sequence 29, Appl 2 Sequence 4, Appl 3 Sequence 498, Appl 2 Sequence 498, Appl 2 Sequence 498, Appl 2 Sequence 498, Appl 3 Sequence 498, Appl 3
10 US-09-767-041-51 10 US-09-924-358-29 9 US-09-738-626-3905-99 10 US-09-765-272-196 10 US-09-765-272-196 10 US-09-765-272-196 10 US-09-765-272-126 10 US-09-906-038A-1 10 US-09-9815-272-122 10 US-09-915-272-202 10 US-09-915-272-202 10 US-09-915-272-202 10 US-09-915-272-202 10 US-09-915-272-202 10 US-09-915-272-202 10 US-09-915-272-202 10 US-09-915-27-91 10 US-09-915-27-91 11 US-10-074-527-4 12 US-10-074-527-4 12 US-10-074-527-4 12 US-10-074-527-4 12 US-10-074-527-4 13 US-09-978-598-498 9 US-09-978-192A-498 9 US-09-978-192A-498 9 US-09-978-192A-498
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189.5 187 177 176.5 173.5 168.5 168.5 164.5 153 153 153 145.5 145.5 145.5 137.5 137.5 137.5 137.5 137.5 137.5 137.5 137.5
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ALIGNMENTS

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Sequence 10, Application US/09879959

Fatent No. US2002016048941

GENERAL INFORMATION:
APPLICANT: Weigel, Paul H

APPLICANT: Rumari, Kshama
APPLICANT: DeAngelis, Paul
TITLE OF INVENTION: STREPTCOCCUS EQUISIMILIS HYALURONAN SYNTHASE GENE AND EXPRESS:
TITLE OF INVENTION: BACILLUS SUBTILIS
TITLE OF INVENTION: NUMBER: US/09/879,959
CURRENT APPLICATION NUMBER: 09/469,200
FRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 10

SOFTWARE: PATENTI OF SEQ ID NOS: 10

SOFTWARE: PATENTI OF SEQ ID NOS: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 KDFPKDLVLAPLPDHVNDFTWYKRKKKIGIKPEHQHVGLSIIVTTFNRPAILSITLACL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 EDKKNSVCDSSLDIATQLLLSNVKKLTLSESEKNSLKNKWKSITGKKSENAEIRKVELVP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 KDFPKDLVLAPLPDHVNDFTWYKNRKKSLGIKPVNKNIGLSIIIPTFNRSRILDITLACL 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: pasteurella multocida
US-09-879-959-10
RESULT 1
US-09-879-959-10
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LENGTH: 972
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                                     294 ETATINNIPSITSKGNISLDWRLEHFKKTDNLRLCDSPFRYFVAGNVAFSKEWLNKVGWFD 353
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                                                                                                          of Essential Genes in
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JAPPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Yaskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Wanamnoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essent:
TITLE OF INVENTION: Prokaryotes
FITLE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4950, Application US/09815242; Patent No. US20020061569A1; GENERAL INFORMATION:
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                                          PRIOR FLIANG DATE: 2000-05-23
PRIOR FLIANG DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR FLIANG DATE: 2000-05-26
PRIOR FLIANG DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLICATION NUMBER: 60/25,931
PRIOR PLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR FLIANG DATE: 2000-12-22
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2010-10-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FRISED FOR WINDOWS VERSION 4.06
PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
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LENGTH: 706
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Sequence 34, Application US/09767041
; Sequence 34, Application US/09767041
; Patent No. US20020055168A1
; GENERAL INFORMATION:
    APPLICAMT: Smith, Hilda
: TITLE OF INVENTION:
    FILE REFERENCE: 2183-4726
    CURRENT APPLICATION NUMBER: US/09/767,041
; CURRENT PELICATION NUMBER: PCT/NL99/00460
; PRIOR APPLICATION NUMBER: PP98202465.5
; PRIOR FILING DATE: 1998-07-19
; PRIOR PLILOR DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: EP98202465.5
; PRIOR PRILING DATE: 1998-07-22
; PRIOR PLILING DATE: 1998-07-22
; PRIOR PLILING DATE: 1998-07-22
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                             -----LVSIIIP-TKNGYKDVQRCVSSIIEKTTYQNYEIIMADNGSTDPKMHELY 489
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  341 ILEEIGGFRKGYEGSQDYDLVLRFTEKTTKERITHIPKVLYYWRMLPTSTAVDQGSKGYA 400
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                                                                                          Query Match 4.8%; Score 246; DB 10;
Best Local Similarity 25.3%; Pred. No. 7e-11;
Matches 92; Conservative 58; Mismatches 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 715;
                                                                                                                                                                                                                                                                                                             APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
  LAINVNYSAVTAACLLMKKADFDAVGGFEEAFTVAFNDVDL 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 5.4%; Score 276.5; DB 10; Best Local Similarity 21.5%; Pred. No. 1.2e-12; Matches 151; Conservative 115; Mismatches 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR PAPLICATION NUMBER: 06/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PLICATION NUMBER: 60/207,727
PRIOR PLICATION NUMBER: 60/207,727
PRIOR PLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR PELICATION NUMBER: 60/253,625
PRIOR PELICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-26
PRIOR FILING DATE: 2001-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10511
LENGTH: 715
                                                                                                                              ce 10511, Application US/09815242
No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Enterococcus faecalis
US-09-815-242-10511
                                                                                                                                                                                                                                Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
597
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2183-4726

us-09-842-484a-2.rapb

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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 YVDRENSIITSSMIDHRFHCLLEFQNERMDFYESRGDKEL-LLECYRSFLAFAVLFLGKY 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 KENGGLSDARNYGISRAKGDYLAFIDSDDFIHSEFIQRLHEAIERENALVAVAGYDRVDA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     605 VDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVNQSLNRQGINYY 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     665 NYDKFDDLDES--RKYIFNKTAEYQ-EEMDML-----KDLKLIQNKDAKIAVSIF----Y 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----NVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGFNENIENA 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 SGHFLTAEPLPTNQAVLSGRN----VCKKLLEA-DGHRF----VVAWN-----KL 164
708 VSIFYPNTLNGLVKKLNNIIEYN--KNIFVIILHVDKNHLT--PDIK-KEILAFYHKHQV 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              435 VSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIMS 494
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                           --VKCLNKMYSTDCLDNEFLPILESYRKEIRRYPFIKAKRYLS--RKHLV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :|| :| || |: :|::| :|| :| :|| 4 ISIIVPIYINVEQYLSKCINSIVNQTYKHIEILLIVNDGSTDNSEEICLAYAKKDSRIRYFK 63
                                                                                                                                                                                                                                                                                                A: STREPTOCOCCUS SUIS VACCINES AND DIAGNOSTIC TESTS 2183-4726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            495 KPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDKTLACVYTTNR---
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llarity 24.4%; Pred. No. 3.1e-09;
Conservative 65; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                          FILE KEFERGATION NUMBER: US/09/767,041
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: PCT/NL99/00460
PRIOR FILING DATE: 1999-07-19
PRIOR FILING DATE: 1998-07-22
PRIOR FILING DATE: 1998-07-22
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
LENGTH: 332
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                                                                                                                                                                                                                        Sequence 22, Application US/09767041
Patent No. US20020055168A1
GENERAL INFORMATION:
APPLICANT: Smith, Hilda
TITLE OF INVENTION:
FILE REFERENCE: 2183-4726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Streptococcus suis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: misc_feature
; OTHER INFORMATION: CPS2K
US-09-767-041-22
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TITLE OF INVENTION: ST
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                                              255 -----
                                                                                    763 NILL 766
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301 TLYL 304
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US-09-767-041-36
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Matches
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Sequence 200, Application US/09765272
Patent No. US20020061245A1
GENERAL INFORMATION:
APPLICANT: Choi et. al.
APPLICANT: Choi et. al.
NUMBER OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 YFKKENGGLSDARNYGISRAKGDYLAFIDSDDFIHSEFIQRLHEAIERENALVAVAGYDR 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 ISKISIIVPIYNVEKYLSKCIDSIVNQTYKHIEILLAVNDGSTDNSEEICLAYAKKDSRIR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10; Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS Version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 223.5; DB 1
Pred. No. 2.7e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            4.4%; Sco. No. 2... 34.1%; Pred. No. 2... 29; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/COCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 200:
FILE RELEATED.
CURRENT APPLICATION NUMBER: US/09/767,041
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: PCT/NL99/00460
PRIOR FILING DATE: 1999-07-19
PRIOR FILING DATE: 1998-07-22
PRIOR FILING DATE: 1998-07-22
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.0
SEQ ID NO 36
LENGTH: 278
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FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                    PCT/NL99/00460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Human Genome Scien
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                            ORGANISM: Streptococcus suis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 34.1%
Matches 44; Conservative
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                                                                                                                                                                                                                                                                                                                                                                      ), NAME/KEY: misc_feature
), OTHER INFORMATION: CPS1K
US-09-767-041-36
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228 QLENLEEKTFDLFVKIFGGQYEFSVFKETL-QWHIIYYSLLMFKNGDESLPKKLHIFKYL 286
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                                                                                                                                                                                                                                                                                                                                                                                                                     ----GGLLATFDGNYQESELQKCQIDLEEIKEVRDLGNENFPNHYMSGIFNSPCCKLYK 169
                                                                                                                                                                                                                            495 KPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVE---LCLKEFLKDKTLACVYTTNR 551
                                                                                                  435 VSIYIPAYNCANYIQRCVDSALNOTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIMS 494
                                          Gaps
                                                                                                                                          64 LPNGGVSNARNYGIKNSTANYIMFVDSDDIVDGNIVESLYTCLKE--NDSDLS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/10007267
Patent No. US20020127682A1
GENERAL INFORMATION:
APPLICANT: GOLSCHlich, Emil C.
AAPLICANT: GOLSCHlich, Emil C.
AITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF OLIGOSACCHARIDES, AND GENES ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  680 FNKTAEYQEEMDML--KDLKLIQNKDAKIAVSIFYPNTLNGLVK-KLNNIIEYNKN 732
                                    87;
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0. Version #1.25 CURRENT APPLICATION DATA:
                                    116;
24.2%; Pred. .v..
Hive 67; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/333,412
FILING DATE: 15-0un-1999
APPLICATION NUMBER: 08/312,387
FILING DATE: July 7, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/007,267
FILING DATE: 03-Dec-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 348 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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COUNTRY: USA
Best Local Similarity 24.29
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Hackensack
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -VNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHL------TDGFNENIE 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --LNQKVYL-LSE--KVIYLNKSLYAYRIRKGSLSRVWTEKWMHALVDAMSERITLLANM 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               642 GIQKKNHFVVVNQSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQN 701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----YHKHQVNILLNNDISYYTSNRLIKTEAHLSNINKLSQLNLNCEYIIFDNHDSLFVK 812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:|| :|| ::|: |||||| :|: || ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----AYMKKYDVGMNFSALTHDWIEKIN 840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         702 KDAKIAVSIFYPNTLNGLVKKLNNIIEYNKNIFVIILHVD-KNHLTPDIKKEILAF----
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                                                                                                                                                                                                                                                             Length 674;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 511 AKGYYIGQLDSDDYLEPDAVELCLK---EFLKDKTLACVYTTNRN-
                                                                                                                                                                                                                                                             DB 10;
                                                                                                                                                                                                                                                       4.4%; Score 223.5; DB 10;
ilarity 20.1%; Pred. No. 9.1e-09;
Conservative 89; Mismatches 177;
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Patent No. US20020055168A1
GENERAL INFORMATION:
TITLE OF INVENTION: STREPTOCOCCUS SUIS VAC
FILE REFERENCE: 2183.4726
CURRENT APPLICATION NUMBER: US/09/767,041
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: PCT/NL99/00460
PRIOR PILING DATE: 1999-07-19
PRIOR FILING DATE: 1998-07-19
PRIOR FILING DATE: 1998-07-22
                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 200:
US-09-765-272-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4BER: PCT/NL99/00460
1999-07-19
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PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 53
SCFWARE: Patentin version 3.0
SEQ ID NO 21
LENGTH: 332
   LENGTH: 674 amino acids
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OTHER INFORMATION: CPS2J
                                                                                                                                                                                                                                                                                    Local Similarity
les 96; Conserv
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                                                                        Gaps
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                                                                        48;
                                                                                                                                                                                                                                                                                                                                                                                                                                     241 QKTARRDFL---QSMGFK-----TRFDSLE----YRQTKAAAYELPEKDL 278
                                                                                                                                                                                                                                                                                                                                                                                                             644 QK--KNHFVVVNQSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQ-EEMDM 692
                                   Length 348;
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COMPUTER: IBM PC Compatible
COMPATER: TBM PC Compatible
COMPATER: TBM PC Compatible
COMPATER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/007,267
FILING DATE: 03-Dec-2001
CLASSIFICATION: CURNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/333,412
FILING DATE: 15-Jun-1999
APPLICATION NUMBER: 08/312,387
FILING DATE: 11994
ATTORNEY/AGENT: INFORMATION:
                               Score 210; DB 12;
Pred. No. 3.6e-08;
                                                                      57; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600-1-095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: profein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-007-267-11
                               4.1%; Score 210;
nilarity 26.4%; Pred. No. 3
Conservative 57; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gotschlich, Emil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/10007267
Patent No. US20020127682A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 348 amino acids
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TELEX: 133521
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CORRESPONDENCE ADDRESS:
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                                   Ouery Match
Best Local Similarity
Matches 77; Conserv
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US-10-007-267-3
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                                                                                                                                                                                                                                                                                       546 V--YTTNRNVNPDGSLIA----NGYNWPEFSREKLTTAMI----AHHFRMFTIRAWHLT 594
                                                  Gaps
                                                                                                                                       3 PLVSVLICAINVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLAIAKDFQKRDSRIKI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICAT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
OLIGOSACCHARIDES, AND GENES ENCODING THEM
                                                  48;
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                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
4.1%; Score 210; DB 12;
26.4%; Pred. No. 3.6e-08;
iive 57; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/007,267

FILING DATE: 03-Dec-2001

CLASSIFICATION: «Unknown»

PRIOR APPLICATION NUMBER: US/09/333,412

APPLICATION NUMBER: US/09/333,412

FILING DATE: 15-Jun-1999

APPLICATION NUMBER: 08/312,387

FILING DATE: 10117 7, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTATION NUMBER: 26,742

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-007-267-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 487-5800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/10007267 Patent No. US20020127682A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 201 343-1684
TELEX: 133521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New Jersey
COUNTRY: USA
                              Best Local Similarity 26.4%
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Hackensack
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US-10-007-267-5
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Sequence 39, Application US/09816028A

Factor No. US20020043369A1

GENERAL INFORMATION:

APPLICANT: Glibert, Michel

APPLICANT: National Research Council of Canada

TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of

TITLE OF INVENTION: Campylobacter Glycosyltransferases

CURRENT PRILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: US 60/118,213

PRIOR PELING DATE: 1999-02-01

PRIOR PELING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 49

SECTION NO. 20

SECTIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----VYTTNRNVNPDGSLIANGYNWPEFSREKLTTAMI-----AHHFRMFTIRAWHLTDG 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                          639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 EIRAGYWKAAGIAVGADCLNYGLLKSTAYALYEKALSGQDIGCLRLFLYEYFLSLE---K 297
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                                                                                                                                                                                              433 PLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRI 492
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: glycosyltransferase from C. jejuni OH4384 (ORF 12a CTHER INFORMATION: of lipooligosaccharide (LOS) blosynthesis locus) US-09-816-028A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---FNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIK-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---KLGIQKKNHFVVVNQSLNRQGI----NYYNYDKFDDLDESRK
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                                                                                                                                            Indels
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4.1%; Score 208.5; DB 10;
Best Local Similarity 23.7%; Pred. No. 3.3e-08;
Matches 78; Conservative 54; Mismatches 122;
                                                                                                                                         53; Mismatches 129;
                                                                                  ; DB 12;
4.1e-08;
                                                                               Score 209;
Pred. No. 4.
  SEQUENCE DESCRIPTION: SEQ ID NO: 12:
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ORGANISM: Campylobacter jejuni
                                                                                    4.18;
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                                                                                                                                         Conservative
                                                                                    Query Match
Best Local Similarity
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                          US-10-007-267-12
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                                                                                                            433 PLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRI 492
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                                                                                                                                                                                                                                                              123 AWLEVLSEENNKSVLAAIARNGAIWDKPTRHEDIVAVFPFGNPIHNNTMIMRRS--VIDG 180
                                                             Gaps
                                                                                                                                               -----NYYNYDKFDDLDESRK
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Patent No. US20020127682A1
GENERAL INFORMATION:
GAPPLICANT: GGISCHICH, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF OLIGOSACCHARIDES, AND GENES ENCODING THEM
  Length 337;
                                                          Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin_Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---FNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIK----
4.1%; Score 209; DB 12; 1
23.7%; Pred. No. 4.1e-08;
tive 53; Mismatches 129;
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APPLICATION NUMBER: US/10/007,267
FILING DATE: 03-Dec-2001
CLASSIFICATION OATA:
PRIOR APPLICATION DATA:

APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US/09/333,412
FILING DATE: 15-Jun-1999
APPLICATION NUMBER: 08/312,387
FILING DATE: July 7, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 337 amino acids TYPE: amino acid
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SEQUENCE CHARACTERISTICS:
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STATE: New Jersey
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 YSLTDLLDFLTDRVMRK 314
                                                       Conservative
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                             Similarity
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Query Match
                             Best Loca
Matches
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Sequence 27, Application US/09816028A

Patent No. US20020042369A1

GENERAL INFORMATION:

APPLICANT: Gilbert, Michel

APPLICANT: National Research Council of Canada

TITLE OF INVENTION:

APPLICANT: Mathematical Council of Canada

TITLE OF INVENTION:

APPLICANT: Mathematical Council of Canada

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/816,028A

CURRENT FILING DATE: 2001-03-21

PRIOR FILING DATE: 1099-02-01

PRIOR PLING DATE: 1009-02-01

PRIOR PLING DATE: 1000-01-31

NUMBER OF SEQ ID NOS: 49

SEQ ID NO 27

LENGTH: 301

LENGTH: 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----KKFDFNSGFYSKKEFVKKI-IAKKNLY-------WTMWGKL 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DESRKYIFNKTAEYQEEMDMLKDLKLIQNKDAKIAVSIFYPNTLNGLVKKLNNIIEYNKN 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 IRKKLYL----EAFASLRLEKDVKINMAED-----VLLYYP-----MLSQAQKIAYMNCN 208
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                                                                                                            664 YNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQNKDAKIAVSIFY-PNTLNGLVKK 722
                                                                                                                                         --ENKNKEILNQNYHDKKKSNEIIKK 240
610 FLKLSEVGKF-KHLN----KICYNRVLHGDNTSIKKLGIQKKNHFVVVNQSLNRQGINY 663
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                                                                            166 ILKSFEKIKIDERLNYGEDVLFCYIYFMFCEKIAVFKTCI--
                                                                                                                                              206 YHYE-----FNPNGRY------
                                                                                                                                                                             LNNII---EYNKNIFVIILHVD---KNHL 745
                                                                                                                                                                                               TYPE: PRT ORGANISM: Campylobacter jejuni
                                                                                                                                                                                                                                                            RESULT 14
US-09-816-028A-27
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Sequence 34, Application US/09816028A

Sequence 34, Application US/09816028A

Patent No. US200200423691

GENERAL INFORMATION:

APPLICANT: Gilbert, Michel

APPLICANT: Wakarchuk, Warren W.

APPLICANT: Wakarchuk, Warren W.

APPLICANT: Wakarchuk, Warren W.

TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of TITLE OF INVENTION: Campylobacter Glycosyltransferases

CURRENT APPLICATION UNMER: US 60/118, 213

PRIOR FILING DATE: 1999-02-01

PRIOR FILING DATE: 2001-01-31

PRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 49

SOFTWARE: Patentin Ver: 2.1

SEQ ID NOS: 49
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Best Local Similarity 21.2%; Pred. No. 9.9e-08;
Matches 114; Conservative 81; Mismatches 146;
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Search completed: January 4, 2003, 02:49:25 Job time: 206 secs

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January 4, 2003, 02:23:10 ; Search time 400 Seconds (without alignments) 1555.419 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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	Description	Sequence 2, Appli	Sequence 3, Appli		Sequence 3, Appli	~	•
SUMMARIES	ΙD	PCT-US01-13395-2	PCT-US99-26501-3	PCT-US01-13395-4	PCT-US99-07289-3	PCT-US99-07289-8	US-09-283-402-3
	DB	7	Н	Т	_	ч	16
	Query Match Length DB ID	965	965	965	972	972	972
ďρ	Query	100.0	100.0	9.66	98.6	98.6	98.6
	Score	5089	5089	2067	5017.5	5017.5	5017.5
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Sequence 8, Appli Sequence 3, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 1, Appli Sequence 2714, Appli Sequence 2714, Appli Sequence 6889, Appli Sequence 5714, Appli Sequence 6889, Appli Sequence 5714, Appli Sequence 4950, Appli Sequence 10511, Appli	10511 10511 5087, 16847
6 US-09-283-402-8 US-09-469-200-8 US-09-469-200-8 US-09-469-90-8 US-09-469-90-8 US-09-469-90-8 US-09-469-90-8 US-09-791-537-56855 US-09-791-537-56855 US-09-791-537-18-9 PCT-US99-07289-1 US-09-791-537-118183 US-09-781-718-9 PCT-US99-07289-7 US-09-791-537-118183 US-09-791-537-10 US-09-791-537-10 US-09-791-537-10 US-09-789-7 US-09-80-789-7 US-09-80-789-7 US-09-80-789-7 US-09-80-789-7	US-09-134-000-15US-09-134-0000-134-000-134-000-134-000-134-000-134-000-134-000-134-000-134-0000
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ALIGNMENTS

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Sequence 2, Application PC/TUS0113395
GENERAL INFORMATION:
APPLICAMT: DE ANGELIS, PAUL L.
TITLE OF INVENTION: CHONDROITIN SYNTHASE GENE AND METHODS OF MAKING AND TITLE OF INVENTION: USING SAME
FILE REFERENCE: 618755-9/JP/199,538
CURRENT APPLICATION NUMBER: PCT/US01/13395
CURRENT FILING DATE: 2001-04-25
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTING PAYE: 2000-04-25
LENGTH: 965
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Best Local Similarity 100.
Matches 965; Conservative
RESULT 1
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                                                      PFEVVVADDGSKENLLTIVQKYEQKLDIKYVRQKDYGYQLCAVRNLGLRTAKYDFVSILD
                                                              CDMAPQQLWVHSYLTELLEDNDIVLIGPRKYVDTHNITAEQFLNDPYLIESLPETATNNN
                                                                                          PSITSKGNISLDWRLEHFKKTDNLRLCDSPFRYFVAGNVAFSKEWLNKVGWFDEEFNHWG
                                                                                                                     NKLYGNNPRVRIMSKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKD
      CDSSLIPIATQLLLSNVKKLTLSESEKNSLKNKWKSITGKKSENAEIRKVELVPKDFPKDL
                                  VLAPLPDHVNDFTWYKNRKKSLGIKPVNKNIGLSIIIPTFNRSRILDITLACLVNQKTNY
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GENERAL INFORMATION:
APPLICANT: THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA
TITLE OF INVENTION: POLYMER GRAFTING BY POLYSACCHARIDE SYNTHASES
FILE REFERENCE: 617481-5
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                                                                                         100.0%; Score 5089;
Llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
 APPLICATION NUMBER: PCT/US99/26501
ORGANISM: Pasteurella multocida
                                                                                                  Best Local Similarity
Matches 965; Conserv
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Sequence 3, Application PC/TUS9907289
GENERAL INFORMATION:
APPLICANT: Board of Regents of the University of Oklahoma
TITLE OF INVENTION: NUCLEIC ACID ENCODING HYALURONAN SYNTHASE AND METHODS
TITLE OF INVENTION: OF USE
FILE REFERENCE: 617022-7
CURRENT FADLICATION NUMBER: PCT/US99/07289
CURRENT FILING DATE: 1999-04-01
EARLIER RAPLICATION NUMBER: 60/108,414
EARLIER FILING DATE: 1998-04-02
EARLIER FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SSOFTWARE: PATENTIN OF USE
STATUS FILING DATE: 1098-10-26
NUMBER OF SEQ ID NOS: 29
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Matches 953; Conservative
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APPLICANT: DE ANGELIS, PAUL L.

TITLE OF INVENTION: CHONDROITIN SYNTHASE GENE AND METHODS OF MAKING AND TITLE OF INVENTION: CHONDROITIN SYNTHASE GENE AND METHODS OF MAKING AND TITLE OF INVENTION: USING SAME CURRENT FILING DATE: 2001-04-25

PRIOR APPLICATION NUMBER: 60/199,538

PRIOR PILING DATE: 1999-11-10

PRIOR PILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PATENTIN Ver. 2.1
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ORGANISM: Pasteurella multocida
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        Sequence 8 Application PC/TUS9907289
GENERAL INFORMATION:
APPLICANT: Board of Regents of the University of Oklahoma
TITLE OF INVENTION: NUCLEIC ACID ENCODING HYALURONAN SYNTHASE AND
TITLE OF INVENTION: OF USE
FILE REFERENCE: 617022-7
CURRENT PILING DATE: 1999-04-01
EARLIER APPLICATION NUMBER: 60/080,414
EARLIER APPLICATION NUMBER: 60/080,414
EARLIER APPLICATION NUMBER: 60/178,851
EARLIER FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
VNQKTNYPFEVVVADDGSKENLLTIVQKYEQKLDIKYVRQKDYGYQLCAVRNLGLRTAKY
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      SEQ ID NO 8
LENGTH: 972
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ORGANISM: 1
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                                                      RESULT 6
US-09-283-402-3
Sequence 3, Application US/09283402
Sequence 3, Application US/09283402
Sequence 3, Application Sequence 3, Application Sequence 3, Title OF INVENTION:
TITLE OF INVENTION: MULTOCIDA AND USES THEREOF
TITLE OF INVENTION: MULTOCIDA AND USES THEREOF
FILE REFERENCE: 5820.530
CURRENT APPLICATION NUMBER: US/09/283,402
CURRENT FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver: 2.0
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Pred. No. 0;
5; Mismatches
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; ORGANISM: Pasteurella multocida
US-09-283-402-3
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98.0%;
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Matches 953; Conservative
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Sequence 8, Application US/09283402

SEQUENCE B, Application US/09283402

SEQUENCE B, Application:

APPLICANT: Paul DeAngelis

TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTURELLA

TITLE OF INVENTION: MULTOCIDA AND USES THEREOF

FILE REFERENCE: 5820.530

CURRENT APPLICATION UNMBER: US/09/283,402

CURRENT FILING DATE: 1999-04-01

NUMBER OF SEO ID NOS: 29
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GENERAL INFORMATION:
APPLICANT: Board of Regents of the
TITLE OF INVENTION: UNCLEIC ACID EN
TITLE OF INVENTION: OF USE
FILE REFERENCE: 617022-7
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; GENERAL INFORMATION:
APPLICANT: Board of Regents of the University of Oklahoma
TITLE OF INVENTION: NUCLEIC ACID ENCODING HYALURONAN SYNTHASE AND
TITLE OF INVENTION: NUCLEIC ACID ENCODING HYALURONAN SYNTHASE AND
TITLE OF INVENTION: OF USE
FILE REFERENCE: 617022-7
CURRENT PAPLICATION NUMBER: US/09/469,200
CURRENT FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/080,414
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 972
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LOCATION: (17)
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LOCATION: (201)
OTHER INFORMATION:
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LOCATION: (158)
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                                                                                                                                                                                                                                                                                                                     VNQKTNYPFEVVVADDGSKENLLIIVQKYEQKLDIKYVRQKDYGYQLCAVRNLGLRTAKY 233
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                                                                                                                                                               Query Match 98.6%; Score 5017.5; Best Local Similarity 98.0%; Pred. No. 0; Matches 953; Conservative 5; Mismatches
CURRENT APPLICATION NUMBER: US/09/469,200
CURRENT FILING DATE: 1999-12-21
FINIOR APPLICATION NUMBER: 60/080,414
PRIOR FILING DATE: 1998-04-02
FRIOR APPLICATION NUMBER: 60/178,851
FRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver: 2.0
SEQ ID NOS 2
                                                                                                                    TYPE: PRT ORGANISM: Pasteurella multocida (PmCS)
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Sequence 9, Application PC/TUS9907289

Sequence 9, Application PC/TUS9907289

GENERAL INFORMATION:

APPLICANT: Board of Regents of the University of Oklahoma

TITLE OF INVENTION: NUCLEIC ACID ENCODING HYALURONAN SYNTHASE AND METHODS

TITLE OF INVENTION: OF USE

FILE REFERENCE: 617022-7

CURRENT PLILIG DATE: 1999-04-01

EARLIER APPLICATION NUMBER: 60/080,414

EARLIER FILING DATE: 1998-04-01

EARLIER PILING DATE: 1998-10-26

NUMBER OF SEQ ID NOS: 29

SOFTWARRE: PATENTIN VET. 2.0

SOFTWARRE: PATENTIN VET. 2.0
                                                                          953
                                                                                                      IDSVPEYNTEDIWFQFALLILEKKTGHVFNKTSTLTYMPWERKLQWTNEQIQSAKKGENI
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Sequence 9, Application US/09283402

GENERAL INFORMATION:

APPLICANT: Paul DeAngelis

TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTURELLA

TITLE OF INVENTION: MULTOCIDA AND USES THEREOF

FILE REPERENCE: 5820.530

CURRENT APPLICATION NUMBER: US/09/283,402

CURRENT FILING DATE: 1999-04-01

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PATCHIN Ver. 2.0
KDFPKDLVLAPLPDHVNDFTWYKNRKKSLGIKPVNKNIGLSIIIPTFNRSRILDITLACL 173
           TSNRLIKTEAHLSNINKLSQLNLNCEYIIFDNHDSLFVKNDSYAYMKKYDVGMNFSALTH
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) LOCATION: (952)

) OTHER INFORMATION: either Asn, Asp, Glu or Gln

PCT-US99-07289-9
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90.4%; Score 4601.5;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 874; Conservative 28; Mismatches
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NAME/KEY: MOD_RES
LOCATION: (316)
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ION: (253)
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LOCATION: (292)
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LOCATION: (329)
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LOCATION: (405)
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LOCATION: (243)
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DESCRIPTION
NAME/KEY: MOD_RES
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LOCATION: (201)
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LOCATION: (206)
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OTHER INFORMATION: 6
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LOCATION: (340)
OTHER INFORMATION: 6
NAME/KEY: MOD_RES
LOCATION: (405)
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KEY: MOD_RES
ION: (225)
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KEY: MOD_RES
ION: (233)
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OTHER INFORMATION:
NAME/KEY: MOD_RES
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OTHER INFORMATION:
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LOCATION: (158)
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NAME/KEY: MOD_RES
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                                                                                     DB 16; Length 972;
                                                                                                               7;
                                                                                                               Indels
                                                                                                               63;
                                                either Asn, Asp, Glu or Gln
                                                                                    90.4%; Score 4601.5; 89.9%; Pred. No. 0;
                                                                                                               28; Mismatches
             either Ile or Val
                                                                                                             874; Conservative
                                                                                                 Similarity
             OTHER INFORMATION:
                                               OTHER INFORMATION:
                       NAME/KEY: MOD_RES
LOCATION: (952)
LOCATION: (744)
                                                           US-09-283-402-9
                                                                                     Query Match
                                                                                                   Best Local
Matches 87
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                                                                                                                        Sequence 9, Application US/09469200

Sequence 9, Application US/09469200

GENERAL INFORMATION:

APPLICANT: Board of Regents of the University of Oklahoma

TITLE OF INVENTION: UNCLEIC ACID ENCODING HYALURONAN SYNTHASE AND METHODS

TITLE OF INVENTION: OF USE

FILE REFERENCE: 617022-7

CURRENT APPLICATION NUMBER: US/09469,200

CURRENT FILING DATE: 1998-12-21

PRIOR APPLICATION NUMBER: 60/080,414

PRIOR PILING DATE: 1998-10-26

PRIOR FILING DATE: 1998-10-26

NUMBER OF SEQ ID NOS: 29

SOFUR NO 9

SEQ ID NO 9

SEQ ID NO 9
901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKTSTLTYMPWERKLQWTNEQIXSAKRGENI 960
                                                                                                                                                                                                                                                                                                                                                                                                             Description of Artificial Sequence: consensus
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ORGANISM: Artificial Sequence
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                                PVNKFIINSITL 965
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OTHER INFORMATION: ENAME/KEY: MQD_RES
LOCATION: (479)
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LOCATION: (192)
OTHER INFORMATION: 6
NAME/KEY: MOD_RES
LOCATION: (201)
OTHER INFORMATION: 6
NAME/KEY: MOD_RES
LOCATION: (206)
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LOCATION: (158)
OTHER INFORMATION: 6
NAME/KEY: MOD_RES
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LOCATION: (211)
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NAME/KEY: MOD_RES
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LOCATION: (62)
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US-09-469-200-9
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LOCATION:
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                                            or Gln
                                                                                            Gln
                                                                                                                                                                                                                                                                                 either Asn, Asp, Glu or Gln
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Similarity 89.9%; Pred. No. 0;
                                                                                             or
                                              Glu
                                                                                            either Asn, Asp, Glu
                                                                        LOCATION: GOLLARD LOCATION: GOLDER INFORMATION: Gither Asn, Asp, Glunamics: MAME/KES: MOD_RES
LOCATION: (316)
OTHER INFORMATION: Gither Ile or Val
NAME/KEY: MOD_RES
LOCATION: (329)
OTHER INFORMATION: Gither Phe or Tyr
NAME/KEY: MOD_RES
LOCATION: (340)
OTHER INFORMATION: Gither Phe or Tyr
NAME/KEY: MOD_RES
LOCATION: (405)
OTHER INFORMATION: Gither Asn, Asp, Glunamics: MOD_RES
LOCATION: (405)
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                                              Asn, Asp,
either Ile or
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                                              either
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                                                                 VPYIYRKLLPIEDSHIHRIPLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGST
                                                                                                                   VPYIYRKLLPIEDSHINRVPLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGST
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GENERAL INFORMATION:
APPLICANT: Weigel, Paul H.
APPLICANT: Weigel, Paul H.
APPLICANT: LoeAngelis, Paul
TITLE OF INVENTION: Hyaluronan Synthase Gene and
TITLE OF INVENTION: Hyaluronan Synthase Gene and
FILE REPERENCE: 3554.011.768B
CURRENT APPLICATION NUMBER: US/10/011,768B
CURRENT FILING DATE: 1998-10-26
PRIOR FILING DATE: 1998-10-26
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: US 60/064,435
PRIOR FILING DATE: 1997-10-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATCHIN VERSION 3.1
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US-10-011-768B-9
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BLONOMLX, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 56855
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88.3%; Score 4493.5;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 844; Conservative 61; Mismatches
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; ORGANISM: Pasteurella multocida
US-09-791-537-56855
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                                                 EDKKNSVCDSSLDIATQLLLSNVKKLTLSESEKNSLKNKWKSITGKKSENAEIRKVELVP 113
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 972;
             7;
 Length
             60; Indels
 DB 24;
88.2%; Score 4490.5;
86.7%; Pred. No. 0;
iive 62; Mismatches
       Local Similarity '86.7 tes 843; Conservative
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        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Weatgel., Paul H.
APPLICANT: Weatgel.s, Paul H.
APPLICANT: Kumari, Kshama
TITLE OF INVENTION: Hyaluconan Synthase Gene and
FILE REFERENCE: 354.011
CURRENT APPLICATION NUMBER: US/10/011,771B
CURRENT FILING DATE: 2001-10-11
PRIOR FILING DATE: 1998-10-26
PRIOR FILING DATE: 1998-10-26
PRIOR FILING DATE: 1998-10-26
PRIOR FILING DATE: 1997-10-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
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Pred. No. 0;
12; Mismatches
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86.7%; Pred
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4, 2003, 02:24:29; Search time 562 Seconds
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121.219 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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101 PSITSKGNISLDWRLEHFKKTDNLRLCDSPFRYFVAGNVAFSKEWLNKVGWFDEEFNHWG 360

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พิพิพัพพพพพพพพพพพพพพพพ พ	A-2 Application US/(ORMATION: DEMACELIS, PAUL NVENTION: CHONDR ELENCE: 4605.03 PLICATION NUMBER: LING DATE: 2001- LICATION NUMBER: SEQ ID NOS: 7 Patentin version 65 Pasteurella mult A-2	100 Conservative Conservative LIKAYNSNDYELA LITHIHIHIHIHIL LIKAYNSNDYELA ATQLLLSNVKKL HIHIHIHIHIHIH ATGLLLSNVKKL ATGLLLSNVKKL HIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI
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८ 8501084996889	SULT 1 -09-842-484A-2 Sequence 2, Application US/09842484A GENERAL INFORMATION: TITLE OF INVENTION: CHONDROITIN SYNTHA FILE REFERENCE: 4605.003 CURRENT APPLICATION NUMBER: US/09/842, CURRENT FILING DATE: 2001-04-25 PRIOR FILING DATE: 2000-04-25 NUMBER OF SEQ ID NOS: 7 SOFTWARE: PATENTIN NUMBER: 05/199,538 PRIOR FILING DATE: 2000-04-25 NUMBER OF SEQ ID NOS: 7 SEQ ID NO 2 LENGTH: 965 TYPE: PRT ORGANISM: PASTEUTELIA multocida ORGANISM: PASTEUTELIA multocida	Query Match Best Local Similarity Matches 965; Conser 1 MNTLSQAIKAYNS 1 MNTLSQAIKAYNS 61 CDSSLDIATQLLL 111111111111111111111111111111111
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TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/10/217,613
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 09/283,402
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SEQUENCE 4, APPLICATION US/09842484A
GENERAL INFORMATION:
TELECANT: DEANGELIS, PAUL L.
TITLE OF INVENTION: US/09/842,484A
CURRENT PELICANTION UNMBER: 02/09/842,484A
CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/199,538
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VEFSION 3.1
SEQ ID NO 666
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960; Conservative 2; Mismatches
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Sequence 8, Application US/10217613

GENERAL INFORMATION:
APPLICANT: DEANGELIS, PAUL
TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTURELLA MULTOCIDA AN
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 35541.081
CURRENT PAPLICATION NUMBER: 09/283,402
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-04-02
PRIOR FILING DATE: 1998-04-02
PRIOR FILING DATE: 1998-04-02
PRIOR FILING DATE: 1998-10-26
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 9
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llarity 99.5%; Pred. No. 0;
Conservative 2; Mismatches
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US-10-217-613-8
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LENGTH: 965
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                                                                                                                                                                              2; Mismatches
                                                                                                                                                       Score 5067;
Pred. No. 0;
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/080,414
PRIOR FILING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: 09/178,851
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VECSION 3.1
SEQ ID NO 3
                                                                                                        TYPE: PRT
ORGANISM: Pasteurella multocida
                                                                                                                                                       99.68;
99.58;
                                                                                                                                                   Query Match
Best Local Similarity 99.5'
Matches 960; Conservative
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or Gln
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OTHER INFORMATION: either Asn, Asp, Glu or Gln
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OTHER INFORMATION: either Asn, Asp, Glu or Gln
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OTHER INFORMATION: either Asn, Asp, Glu
FEATURE:
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OTHER INFORMATION: either Asn, Asp, Glu
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LOCATION: (243)..(243)
OTHER INFORMATION: either Ile or Val
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OTHER INFORMATION: either 11e or Val
FEATURE:
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OTHER INFORMATION: either Ile or Val
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OTHER INFORMATION: either Ile or Val
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OTHER INFORMATION: either ile or Val
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OTHER INFORMATION: either Phe
                                       LOCATION: (113)..(113)
OTHER INFORMATION: either Ile
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OTHER INFORMATION: either
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OTHER INFORMATION: either
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OTHER INFORMATION: either
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OTHER INFORMATION: either
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OTHER INFORMATION: either
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TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTURELLA MULTOCIDA AND US
TITLE OF INVENTION: THEREOF
FILE EFFERENCE: 35541.081
CURRENT PILICATION NUMBER: US/10/217,613
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 09/283,402
PRIOR APPLICATION NUMBER: 06/080,414
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/080,414
PRIOR APPLICATION NUMBER: 09/178,851
PRIOR PELING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 9
LENGTH: 972
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NKLYGNNPRVRIMSKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKD 540
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LOCATION: (90)...(90)
OTHER INFORMATION: either Asn, Asp, Glu or Gln
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NAME/KRY: MISC_FEATURE
LOCATION: (17)..(17)
OTHER INFORMATION: either Asn, Asp,
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OTHER INFORMATION: either Asn, Asp,
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|NSITL 965
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US-10-217-613-9
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APPLICANT: DeAngells, Paul H.
APPLICANT: DeAngells, Paul
APPLICANT: Consequence of the consequence o
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; GENERAL INFORMATION:
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Matches 843; Conservative
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US-09-469-200D-9
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NAME/KEY: MISC_FEATURE
LOCATION: (952)..(952)
UCHER INFORMATION: either Asn,
US-10-217-613-9
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Best Local Similarity 89.97
Matches 874; Conservative
                                              FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (744)..(744)
OTHER INFORMATION: either
              LOCATION: (439)..(439)
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MISC_FEATURE
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GENERAL INFORMATION:
APPLICANT: WEIGEL, PAUL H
APPLICANT: WEIGEL, PAUL H
TITLE OF INVENTION: HYALURONAN SYNTHASES AND METHODS OF MAKING AND USING SAME
TITLE OF INVENTION: HYALURONAN SYNTHASES AND METHODS OF MAKING AND USING SAME
TITLE OF INVENTION: HYALURONAN SYNTHASES AND METHODS OF MAKING AND USING SAME
CURRENT APPLICATION NUMBER: US/10/309,560
CURRENT APPLICATION NUMBER: 60/336,105
PRIOR APPLICATION NUMBER: 60/336,105
PRIOR APPLICATION SOS 92
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patentin version 3.1
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86.6%; Pred. No. 0;
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APPLICANT: DENDELIS, PAUL
TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTURELLA MULTOCIDA AND
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 35541.081
CURRENT APPLICATION NUMBER: US/10/217,613
CURRENT FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/080,414
PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-04-02
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 9
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EEFNHWGGEDVEFGYRLFAKGCFFRVIDGGMAIHQEPPGKENETEREAGKSITLKIVKEK
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GENERAL INFORMATION:
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APPLICANT: SUGIURA, NOBUO
APPLICANT: KIMATA, KOJI
TITLE OF INVENTION: CHOUDROITIN POLYMERASE AND DNA ENCODING THE SAME
FILE REFERENCE: 226882USO
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                    09/178,851
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                                                                                                                                                           Pasteurella multocida
                                                                            version 3.1
PRIOR FILING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: 09/1
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                   al Similarity 82.6
581; Conservative
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Best Local S:
Matches 581
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82.6%; Pred. No. 1.5e
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                                                                              multocida
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                                                                          ORGANISM: Pasteurella
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581; | Conserv
    SOFTWARE: Patentin
                  SEQ ID NO 1
LENGTH: 703
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APPLICANT: NINOMIYA, TOSHIO
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ilarity 61.3%; Pred. No. 9.8e-207;
Conservative 112; Mismatches 148;
CURRENT APPLICATION NUMBER: US/10/216,289
CURRENT FILING DATE: 2002-11-04
PRIOR APPLICATION NUMBER: UP 2001-244685
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: UP 2001-324127
PRIOR APPLICATION NUMBER: UP 2002-103136
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
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US-10-216-289-2
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LENGTH: 686
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US-10-216-289-4
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Sequence 4, Application US/10216289 GENERAL INFORMATION:

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APPLICANT: KIMATA, KOJI
TITLE OF INVENTION: CHONROTIIN POLYMERASE AND DNA ENCODING THE SAME
FILE REFERENCE: 226882USO
CURRENT APPLICATION NUMBER: US/10/216,289
CURRENT FILING DATE: 2002-11-04
PRIOR APPLICATION NUMBER: JP 2001-244685
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-02-2
PRIOR FILING DATE: 2001-02-2
PRIOR FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
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Matches 419; Conserv
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-----IWAGYTQKYAAFDYNVRIL 782
755 AFYHKHQVN------ILLNNDISYYTSNRLIKTEAHLSNINKLSQLNLNCEYIIFDN 805
                                    --ASGVIDFVYMGDNTKII---- 716
                                                                          HDSLFVKNDSYAYMKKYDVGMNFSALTHDWIEKINAHPPFKKLIKTYFNDNDLRSMNVKG 865
                                                                                                              -----EKG 745
                                                                                                                                                    866 ASQGMFMKYALPHELL--TIIKEVITSCQSIDSVPEYNTEDIW------FQFALLIL 914
                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
APPLICANT: Havukkala, Ilkka J
APPLICANT: Havukkala, Ilkka J
APPLICANT: Unbers, Mark William
APPLICANT: Lobers, Mark William
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: them, and methods for using them.
FILE REFERENCE: 11000.1043c3
CURRENT FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 152
LENGTH: 331
                                                                                                                                                                                                                               915 EKKTGHVFNKTSTLTYMPWERKLQWTNEQIQSAKKGENIPVNKFIINSIT 964
                                                                                                                                                                                                                                                               783 TSREGE-----THFSVVRQNQGYIQDTMTSIGNELTPINKIEGNEPT 824
                                                                                                      717 HDSLLVS----LLIKKEGTTLKSIVLQAEW-----
                                                                                                                                                                                         ----YTLLQENMYYTFVDNVFT-----
                                    673 FGQEKTQGNGTAIEMFSIIIADND----TSN-
                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 152, Application US/10264213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Lactobacillus rhamnosus
US-10-264-213-152
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US-09-134-000C-5087
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Best Local Simi
Matches 87;
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US-10-264-213-152
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                                                Sequence 5749, Application US/09134000C
GRNERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES AND THERAPEUTICS
FILE REPERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR PELING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 5749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               501 ASASNAAVSFAKGYYIGQLDSDDYLE------PDAVELCLKEFLKDKTLAC 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 KNIGLSIIIPTFNRSRILDITLACLVNQKTNYPFEVVVADDGSKENLLTIVQKYEQKLDI 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --FVAGNVA------FSKEWLNKVGWFDEEFNHWGGEDVEFGYRLFAKGCFFRVI 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 FKLIRSNLIEQNKFERYKGYFYKQMFEKYFWAIEKLTHLRDESV---YEVIQK----VAV 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIMSKPNGGI 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                            267; Gaps
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ENVTWDEEIKSYGDIGLFWKINSASQNVIFIKDCLYFYRQDNPNSTVNNVATKVPFLFQQ
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                                                                                                                                                                                                                                                                                                                                                                                                  6.6%; Score 333.5; DB 5; 20.8%; Pred. No. 7e-23;
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                                                                                                                                                                                                                                                                                                                                              ORGANISM: Enterococcus faecalis
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                                                                                                                                                                                                                                                                                                                                                                                                              NYKNGKIQINLYECPAVLDSHTAVKRLLYDDQIDTSVWAKLYPAWVFKKIHFPKGRLFE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NVNPDGSLIANGYNWPE------FSREKLTTAMIAHHFRMFTIRAWHLTDG-FNE 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       600 NIENAVDYDMFLKLSEV---GKFKHLNKICYNRVLHGDNTSIKKLGI------QKKN 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            648 HFVVVVNQSLNRQGINYY----NYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLKL-IQN 701
                                                                                                                                                                                                                                             492 IMSKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDKTLACVYTTNR 551
                                                                                                                        IPLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVR 491
                                                                                                                                                          Gaps
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GENERAL INFORMATION:
SPPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
      Length 331;
5.9%; Score 299; DB 6; Length 33:
ilarity 27.9%; Pred. No. 2.7e-20;
Conservative 58; Mismatches 131; Indels
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CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT PELLING DATE: 1999-08-13
PRIOR PILIOR DATE: 1997-08-15
PRIOR FILING DATE: 1997-08-15
SUTHER FOR FILING DATE: 1997-08-15
SOFTWARE: PATCHILN VERSION 3.1
                                                                                                                                                                                                                                             22;
 ENTEROCCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   530 VELCLKEFLKDKTLACVYTINRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIR 589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKNHFVVVNQSLNRQGINYYN-----YDKFDDLDESRKYIFNKTAEYQEEMDMLKDL 696
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                                                                                                                                                                                                                                                                                                                                                                73 NQIYQTEPAIEAGFVVTLEGIKQKKVL----PFHFQSSAHVITVDFPLNKKYPVIPGTE 127
                                                                                                                                                                                                                                                                                                                                                                                                DEEFNHWGGEDVEFGYRLFAKGCFFRVIDGGMAIHQEPPGKENETEREAGKSITLKIVKE 412
                                                                                                                                                                                                                                                                                                                                                                                                                 413 KVPYIYRKLLPIEDSHIHRIPLVSIYIPAYNC-ANYIQRCVDSALNQTVVDLEVCICNDG 471
                                                                                                                                                                                                                                                                                                                                     -----LEHFKKTDNLRLCDSPFRYFVAGNVAFSKEWLNK-----VGWF 352
                                                                                                                                                                                                                                                                         260 DNDIVLIGPRKYVD--THNITAEQFLNDPYLIESLPETATNNNPSITSKGNISLDWR--- 314
                                                                                                                                                                                                                                                                                               590 AWHLTDGFNENIENAVDYDMFLKLSE---VGKFKHLNKICYNRVLHGDNTSIKK--LGIQ
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                                                                                                                                                                                                                                              Indels 111;
                                                                                                                                                                                                               Length 534;
                                                                                                                                                                                                               5.2%; Score 262.5; DB 5;
larity 23.0%; Pred. No. 1.9e-16;
Conservative 100; Mismatches 234;
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RESULT 15
1009-134-000C-6392
1 Sequence 6392, Application US/09134000C
1 GENERAL INFORMATION:
                                                                                                                                                         erococcus faecalis
87
                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Ent
US-09-134-000C-50
                                                                                                                                                                                                                                  Best Local Sim
Matches 133;
                                                                                                                                                                                                                   Query Match
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549 INRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGFNENIENAVDYD 608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          663 YYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQNKDAKIAVS----IFYPNTL-- 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                        432 IPLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVR 491
                                                                                                                                                                                                   492 IMSKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLK---DKTLACVYT
                                                                                                                                                                                                                                                                                                                                                                                                    509 MFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVNQSLNRQGIN-----
                                                                                                      Length 330;
                                                                                                                                                                                                                                                                                                                                                    127 VYEGKEPIVKSLIQG----TFSREEALLLILQGN--IISVHA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----NGLVKK-LNNIIEYNKNIFVIILHVDKNHLTPDIKK 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5;
                                                                                                                                           63; Mismatches 125;
                                                                                                      Score 248.5; DB 5
Pred. No. 1.8e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: January 4, 2003, 02:45:48 Job time : 565 secs
                                TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                  4.9%;
                                                                                                                                           85; Conservative
                                                                                                        Query Match
Best Local Similarity
Matches 85; Conserv
                                                                   US-09-134-000C-6392
SEQ ID NO 6392
                 LENGIH:
                                                                                                                                                                                                                                                                                              29
                                                                                                                                                                                                                                                                                                                                                                                                                                               163
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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January 4, 2003, 02:18:59 ; Search time 69 Seconds (without alignments) 1344,489 Million cell updates/sec Run on:

US-09-842-484A-2 5089 1 MNTLSQAIKAYNSNDYELAĻ......SAKKGENIPVNKFIINSITL 965 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	qlucuronosyltransf	hypothetical prote	ဟ	hypothetical prote	hypothetical prote	glycosyltransferas	qlycosyltransferas	hypothetical prote	hypothetical prote		hypothetical prote	glycosyl transfera	beta-1,3-N-acetylg	hypothetical prote	teichuronic acid b	capsular polysacch	minor teichoic aci	hypothetical prote	glycosyltransferas	glycosyl transfera	hypothetical prote	glycosyltransferas	lacto-N-neotetraos	probable sugar tra			tran		probable requiator
SUMMARIES	ΩI	95	E97757	AB1211	D95206	AD2189	A84114	B97168	AG2188	AB2190	B75096	AH2026	T44330	T50038	AE2189	E84107	A70037	E71690	AH2189	A97168	T44647	AE1876	Н97167	D81027	F81289	E81318	н69814	S70813	H64130	E91190
	DB	7	7	~	7	~	7	7	~	7	7	7	~	~	7	~	~	-	~	7	7	~	7	7	7	٦.	7	Н	Н	~
	Query Match Length	972	604	327	969	323	303	333	321	324	298	333	340	306	316	257	344	318	318	336	322	1013	333	349	176	389	392	333	323	338
di	Query Match	88.2	5.8	5.7	5.3	5.2	5.1	5.1	5.0	5.0	4.9	4.7	4.7	4.7	4.7	4.7	4.7	4.6	4.6	4.6	4.6	4.6	4.6	4.5	4.5	4.5	4.5	4.5	4.4	4.4
	Score	4486.5	294	292.5	268.5	264.5	261.5	258.5	256	254.5	251	241	239	238	238	237.5	237	235.5	235	234.5	234	233.5	232	229.5	229.5	229	228	227.5	224.5	223.5
	Result No.	-	7	m	4	5	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

probable regulator beta-1,4-qalactosy	hypothetical prote	hypothetical prote	glycosyltransferas	probable sugar tra	probable glycosyl	hypothetical prote	hypothetical 40.5K	probable glycosylt	probable galactosy	lacto-N-neotetraos	glycosyl transfera	probable two-domai	glycosyl transfera	hypothetical prote
F86037 T50039	AH2188	G71153	E97083	B81289	AG0023	AG2189	ОЗЕСТН	G95948	C81318	н81970	F95205	B81318	A64099	AI2404
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338 318	330	334	338	445	329	318	344	367	390	346	301	515	250	313
4 4	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.2	4.2	4.2	4.2	4.2	4.2
223.5 223	221	221	221	220.5	220	218.5	217.5	217	216	215.5	214.5	214.5	214	214
		33					_	_	_			_		

ALIGNMENTS

RESULT 1	
glucurono N; Alterna	glucuronosyltransferase (EC 2.4.1.17) - Pasteurella multocida N.N.lterate names: hyalurona synthase
C; Date: 1	C.bate: 16-marculeira muirocida C.bate: 16-marculeir1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000 C.bacesion: m09595
R; DeAngel	
 A; Title: A; Referen	A;Tile: identification and molecular cloning of a unique hyaluronan synthase from F A;Reference number: 216757; MUID:98192645; PMID:9525958
 A; Accessi A; Status:	A,Accession: T09595 A,Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecul A; Residue	A;Molecule type: DNA A;Residues: 1-972 <dea></dea>
A; Cross-r	eferences: EMBL:AF036004; NID:93043922; PIDN:AAC38318.1; PID:93043923
C, Genetics:	
A; Gene: HAS C; Function:	A5 n:
 A; Descrip C; Keyword	A;Description: polymerizes hyaluronan (HA, hyaluronate, hyaluronic acid) polysacchar C;Keywords: capsule synthesis; glycosyltransferase; hexosyltransferase; hyaluronic a
 Query M	Query Match 88.2%; Score 4486.5; DB 2; Length 972;
 Matches	Cal Similarity 50.00, Figure 200, 100 100 17; Gaps 2; 842; Conservative 63; Mismatches 60; Indels 7; Gaps 2;
0y 1	1 MNTLSQAIKAYNSNDYELALKLFEKSAETYGRKIVEFQIIKCKEKLSTNSYVS 53
Db 1	MNTLSQAIKAYNSNDYQLALKLFEKSAEIYGRKIVEFQITKCQEKLSAHPSVNSAHLSVN 60
Qy 54	
Db 61	KEEKVNVCDSPLDIATQLLLSNVKKLVLSDSEKNTLKNKWKLLTEKKSENAEVRAVALVP 120
Qy 114	
Db 121	XDFPKDLVLAPLPDHVNDFTWYKKRKKRLGIKPEHQHVGLSIIVTTFNRPAILSITLACL 180
Qy 174	VNQKTNYPFEVVVADDGSKENLLTIVQKYEQKLDIKYVRQKDYGYQLCAVRNLGLRTAKY 233
Db 181	
 Qy 234	
 Db 241	DFIGLLDCDMAPNPLWVHSYVAELLEDDDLTIGPRKYIDTQHIDPRDFLNNASLLESLP 300
 Qy 294	
Db 301	EVKTNNSVAAKGEGTVSLDWRLEQFEKTENLRLSDSPFRFFAAGNVAFAKKMLNKSGFFD 360
 Qy 354	EEFNHWGGEDVEFGYRLFAKGCFFRVIDGGMAIHQEPPGKENETEREAGKSITLKIVKEK 413

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G; Species: Listeria monocytogenes
G; Species: Listeria monocytogenes
G; Species: Listeria monocytogenes
C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
G; Accession: AB1211
G; Accession: AB121
B; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Authors: Kreft, J.; Sinnes, L.M.; Karst, O.
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Alitle: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID: 21537279; PMID: 11679669
A; Accession: AB121
A; Accession: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:NC_003210; PIDN:CAC99168.1; PID:g16410492; GSPDB:GN00177 A;Experimental source: strain EGD-e C;Genetics: A;Gene: lmo1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRI 492
                                                                                                                                                                                                                                                                                                                                                                                                     811
                                                                                                                                                                                                                                                                                                                                                                                                                                                   385
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                                                                                                                                                                                                                                                                                                   LIQNKDAKIAVSIFYPNTLNGLVKKLNNI-IEYNKNIFVIILH----VDKNHLTPDIKKE 752
                                           MSKPNGGIASASNAAVSFAKGYYIGQIDSDDYLEPDAVELCLKEFLKDKTLACVYTTNRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----NENIENAVDY---DMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VNPDGS------LIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGF---
                                                                                                                                                                                                                                        | : : | | : : | | : : | ECNVLWSSFLHELTEEEMIKMEGSPYL-----FLTRTATFLSNNT-PYKKACDLANTWA
                                                                                                                                                                                                                                                                                                                                    :: :: |:|
                                                                                                                                        -ILAFYHKHQVNILLNNDISYYTSNRLIKTEAHLSNINKLSQLNLNCEYIIFDNHDSLFV
                                                                                                                                                                                                                                                                                                                                                                                                                               : ::|| : | | : | | : | | 347 KRIKYEHK-------KNEGPAAARN-LGIKNAIGKYIAFLDSDDLFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              812 KNDSYAYMKKYDVGMNFSALTHDWIEKINAHPPFKKLIKTYFNDNDLRSMNVKGASQGMF
                                                                                                                                                                                                             647 N------HFVVVNQSLNRQGINYXNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLK
                                                                                                            TIRAWHLTDGFNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKK
            -TINRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 327;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y Match 5.7%; Score 292.5; DB 2; Local Similarity 27.5%; Pred. No. 5.9e-09; hes. 98; Conservative 44; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K-DKIEIQLKFMEENNF-IFSHTSYHKINE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGNVFP-----438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   872 MKYALPHELLTIIKEVITSC
                      LKEFLKDKTLACVY-
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D
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C;Species: Rickettsia conorii
C;Species: Rickettsia conorii
C;Date: 30.Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
C;Accession: E97757
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2039-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    773
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                                                                                                                                                                                                NTLNGLVKKLNNI IEYNKNI FVIVLHVDKNHLTPDIKKEILAFYHKHQVNILLNNDI SYY
                                                                                                  TDGFNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVN
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VPYIYRKLLPIEDSHIHRIPLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGST
                                                                                                                                                                       DNTLEVINKLYGNNPRVRIMSKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELC
                                                                                                                                                                                                                                                                    LKEFLKDKTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.8%; Score 294; DB 2; Length 60
Llarity 24.8%; Pred. No. 1.1e-08;
Conservative 71; Mismatches 213; Indels
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Matches 124; Conserv
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A; Molecule type: DNA
A; Residues: 1-604 <KUR>
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hypothetical protein alr3067 (imported] - Nostoc sp. (strain PCC 7120)
C.Species: Nostoc sp.
A.Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C.Date: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C.Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C.Racession: AD2189
R.Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irit.
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabat
DNA Res. B, 205-213, 2001
A.Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A.Reference number: AB1807; MuID:21595285; PMID:11759840
A.Rocession: AD218
A.Status: preliminary
A.Rolecule type: DNA
A.Residues: 1-323 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycosyltransferase BH3713 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Dac-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: A84114
R;Takami, H; Nakasone, K; Takaki, Y; Maeno, G; Sasaki, R; Masui, N; Fuji, F;
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Actus: preliminary
A;Molecule type: DNA
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A;Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07432.1; GSPDB
A;Experimental source: strain C-125
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:BA000019; PIDN:BAB74766.1; PID:g17132161; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----FDPTLKSCEDWDFYLRLAAKWQFALVKKAQIIYRQ---SPTAMTSKLDVMEK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSIVIERAFNAAPPQLQHLKK-----QSLAWVKFTAQQCLKYNSHKLADIKLAA-KRL 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               432 IPLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVR 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        647 NHFVVVNQSLNRQGINYYNYDKFDDLDESRKYIFNKTAE--YQEEMDMLKDLKLIQNKDA 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMSKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVEL---CLKEFLKDKTLACVYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.2%; Score 264.5; DB 2;
25.4%; Pred. No. 2e-07;
tive 64; Mismatches 116;
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26.5%; Pred. No. 2.7e-07;
tive 60; Mismatches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIAVSIFYPNTL----NGLVKKL 723
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KMAITLYPKNLLEDYTHGLIRKL 302
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A84114
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                                                                                                                                                                                                                                                                hypothetical protein Sp1771 [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Species: O3-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: D95206
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: D95206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE005672; PIDN:AAK75845.1; PID:914973268; GSPDB:GN00164; TIGR:SP4
A;Experimental source: strain TIGR4
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
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                                  ---VNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHL-- 593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      745 LTPDIKKEILAF-----YHKHQVNILLNNDISYYTSNRLIKTEAHLSNINKLSQLNL 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      344 WIKQLNKRLEKFDSEIINCRVTSEQIS-CYKSDISYTVFLRYFIADF----VQEDKALYL 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    686 YQEEMDMLKDLKLIQNKDAKIAVSIFYPNTLNGLVKKLNNIIEYNKNIFVIILHVD-KNH 744
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648 HFVVVNQSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDL---KLIQNKDA 704
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7 ITVIVPVYNVENYLERCLDSIIIQTYKNIEIVVVNDGSTDASGEICKEFSEMDHRILYIE 66
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                                                                                                705 KIAVSIFYPNTLNGLVKKLNNIIEYNKNIFVIILHVDKNHLTPDIKKEILAFYHKH 760
                                                                                                                                  Length 696;
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LIDVTNEWHDKVD 471
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A; Molecule type: DNA
A; Residues: 1-696 <KUR>
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A; October 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C; Accession: AG2188
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaii, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A; A; Recence number: AB1807; MUID:21595285; PMID:11759840
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
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C; Species: Nostoc sp.
A; Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C; Accession: AB2190
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabatan DNA Res. 8, 205-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A; Reference number: AB1807; MUID:21595285; PMID:11759840
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-324 < KUR.
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A; Residues: 1-31 <KUR>
A; Cross-references: GB:BA000019; PIDN:BAB74761.1; PID:g17132156; GSPDB:GN00179
A; Experimental source: strain PCC 7120
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 605 V-DYDMFLKLSEVGKFKHLNK-ICYNRVLHGDNTSIK-----KLGIQKKNHFVVVNQS 655
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VEDWDMWLRIATSYDFKVVKEALVYYR--ORSNSASKNWEAMAHSFAIVIEKAFATASQD 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NVNPDGSLI-----ANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGFNENIENA 604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            492 IMSKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDKTLACVYTTNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.0%; Score 254.5; DB 2;
26.2%; Pred. No. 7.1e-07;
Live 63; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.0%; Score 256; DB 2;
ilarity 27.5%; Pred. No. 5.8e-07;
Conservative 50; Mismatches 118
                                          hypothetical protein alr3062 [imported] - Nostoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Matches 101; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 78; Conserv
                                                                      Species: Nostoc sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glycosyltransferase [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: B9768 R;Nolling, J; Breton, G; Comelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. JB. Bacteriol. 183, 4823-4838, 2001 A;Itle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A;Reference number: A96900; MUID:21359325; PMID:21359325 A;Accession: B97168 A;Status: preliminary A;Molecule type: DMS A;Residues: 1-333 < KUR> A;Cross-references: GB.ABC001437; PIDN:AAK80133.1; PID:g15025169; GSPDB:GN00168 A;Experimental source: Clostridium acetobutylicum ATCC824 C;Genetics: A;Gene: CAC2175
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                                                                                                                                                                                                                                                                                                                                                                                           434 LVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIM 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   604 AVDYDMFLKLSEVG-KFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVNQSLNRQGIN 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 -EGFSSIRDIIQSR-----LEYVKEKLKLKDFSYVIWGASNGGKIAYEKIKEVFPNAK 271
                                                                                                                                                                   549 ---TURNVNPDGSLIANGYNWPE----FSREKL-----TTAMIAHHFRMFTIRAWHLTD 595
                                                                                                                                                                                                    --GFNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVN 653
                                                                                                                                                                                                                                                                                                             167 CGMFDEKLKARQDYDLWI------RVC-----RVC-----QKTLVGVVN 196
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                                                                                                                   62 YHPAKGGNYARNTGIKNAKGEFIAFLDDDDEWMPDKLELQIKEFNQNANVGLVYTGVEII 121
663 YYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLKLI---QNKDAKIA---VSIFYPNT-
                                                                      195 -KPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDKTLACVYT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.1%; Score 258.5; DB 2; 26.4%; Pred. No. 4.4e-07; tive 54; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 TEDYNLWLRAIAKGYKIAMLEEKLMKIRLHNDS----
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Best Local Similarity
Matches 81; Conserv
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272 LNGYIDK 278
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hypothetical protein all1766 [imported] - Nostoc sp. (strain PCC 7120)
C.Species: Nostoc sp.
A.Note: 14-Dec-2001 #text_change 30-Jun-2002
C.Accesion: AH2026
R.Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriy
NARazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabat
DNA Res. 8, 205-213, 2001
A.Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A.Reference number: AB1807; MUID:21595285; PMID:11759840
A.Scatus: preliminary
A.Molecule type: DNA
A.Residues: 1-333 <KUR>
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C;Species: Vibrio cholerae
C;Species: 11-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T44330
B;Yamasaki, S.: Shimizu, T.; Hoshino, K.; Ho, S.T.; Shimada, T.; Nair, G.B.; Takeda, Gene 237, 321-332, 1999
A;Title: The genes responsible for O-antigen synthesis of Vibrio cholerae O139 are c A;Reference number: 222749; MUD:99453293; PMID:10521656
A;Reference number: 222749; MUD:99453293; PMID:10521656
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-340 <-YAM>A;Cross-references: EMBL:AB012957; NID:94115688; PIDN:BAA33634.1; PID:93721684
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A;Note: wblC
C;Superfamily: Neisseria meningitidis glycosyl transferase A
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264 SIAIAPLNLENYMILLKLALDSRTVEYIKRILS 296
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C.Species: Pyrococcus abyssi
C.Species: D0-Jun-2000
C.Species: D0-Jun-20
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                                                                                                                                                                                                                                                                                                                                              119 TIDDKGELLKPFE--PLYEGNVYTDLLLAN------FLTNGSNPLIRKAA----- 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 IRLKKNSGGPIARNIGIKKAKGRFIALLDDDDDEWLPHRLEVQVRKFENLGKEFGVVYGGF 121
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                                                                                                                                                                         VYSYENSRASGARNHGISHAVGDFISFLDADDLWTPDKLELQLSALNNHPEAGVAYSWTY 118
                                                                                                                                                                                                                                                                       NVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGFNENIENAVDYDMFL 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLSEVGKFKHLNKICYNRVLHGDNTSIKK------LGIQKKNHFVVVNQSLNRQGINYY 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 -IASIGEF-----HQILY-DTTLRSGEDWDYWLRLAYKWPFVVVKQ----HQILY- 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLKL-IQNKDAKIAVSIFYPNTLNGLVK-K 722
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1 MPKISVIIPAYNAERTILETINSVLNQTFSDLEIIVINDGSTDRTVEVLQNV--DDARLK
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4.9%; Score 251; DB 2; Length 298
Best Local Similarity 24.3%; Pred. No. 9.8e-07;
Matches 81; Conservative 66; Mismatches 136; Indels
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C) Species: Nostoc Sp.
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A) Note: 14-Dec-2001 #text_change 30-Jun-2002
C) Accession: AE2189
B) Note: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C) Accession: AE2189
B) Note: N
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A;Molecule type: DNA
A;Residues: 1-257 <STO.
A;Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07380.1; GSPDB: A;Experimental source: strain C-125
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A; Experimental source: strain PCC 7120
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105 QQHPEAGV---AYSWTYFMDEQGKSSIPGVSLFFEGDVQAHLLVNNFLASGSNPLIRKQA 161
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                                                                                                                                                                                                      hypothetical protein alr3068 [imported] - Nostoc sp. (strain PCC 7120)
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4.7%; Score 238; DB 2; Length 316
Best Local Similarity 24.5%; Pred. No. 5.5e-06;
Matches 78; Conservative 50; Mismatches 109; Indels
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C; Species: Streptococcus pneumoniae
C; Accession: T50038
R; Kolkman, M.A.B.; Wakarchuk, W.; Nuijten, P.J.M.; van der Zeijst, B.A.M.
Mol. Microbiol. 26, 197-208, 1997
A; Title: Capsular polysaccharide synthesis in Streptococcus pneumoniae serotype 14: mole
A; Reference number: Z25028; MUID: 98043549; PMID: 9383201
A; Reference number: Z25028; MUID: 98043549; PMID: 9383201
A; Reference number: Z25028; MUID: 98043549; PMID: 9383201
A; Residues: preliminary; translated from GB/EMBL/DBJ
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Residues: 1-306
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Experimental source: isolate NCTC 11902; serotype 14
A; Experimental source: isolate NCTC 11902; serotype 14
A; Experimental source: isolate NCTC 11902; serotype 14
A; Pathway: capsular polysaccharide biosynthesis
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                                                                                                                                                                                                                                                                                                                                                    435 VSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIMS 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  495 KPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDK----TLACVY---- 547
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                                                     6 PIISVIMSVYNGEKYLAQAIESIINQTFSDFEFIIVDDGSTDSSLSIIQAYMDKDDRIVL 65
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on:

January 4, 2003, 00:40:24 ; Search time 66 Seconds (without alignments) 606.434 Million cell updates/sec

US-09-842-484A-2 5089 1 MNTLSQAIKAYNSNDYELAL......SAKKGENIPVNKFIINSITL 965 Title: Perfect score: Sequence:

112892 seqs, 41476328 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	otion	rhizobium s	haemophilus	escherichia	haemophilus	bacillus su	anabaena sp	myxococcus	mycoplasma	bacillus su	buchnera ap	borrelia bu	buchnera ap	mycoplasm	ureaplasma			plasmodium	staphylococ	escherichia	salmonella	rhizobium m	clostridium	epifagus vi	saccharomyc	mycoplasma	human herpe	human herpe	methanococc	mycoplasma	saccharomyc	saccharomyc	methanococc	bacillus su
	Description	P55465	057287	P11290	057022	P46918	P22639	050864	P75086	P46917	P57529	051578	P57189	P47271	09pdp4	006366	P16154	P27625	P30195	P77414	P26401	P33697	P46082	000383	P28742	P47306	P30002	P52340	058718	P47534	000402	002773	058295	P39621
SUMMARIES	ID	Y4GI_RHISN	YF78_HAEIN	YIBD_ECOLI	Y868_HAEIN	GGAB_BACSU	YS86_ANASP	RFBC_MYXXA	Y025_MYCPN	GGAA_BACSU	EX5B_BUCAI	EX5B_BORBU	Y087_BUCAI	Y025_MYCGE	DPO3_UREPA	BXEN_CLOBU	TOXA_CLODI	RPC1_PLAFA	EPIB_STAEP	WCAA_ECOLI	RFBV_SALTY	EXOO_RHIME	BXEN_CLOBO	YCF1_EPIVI	KIP1_YEAST	Y060_MYCGE	TEGU_HSV6G	TEGU_HSV6U	RA50_METJA	SYA_MYCGE	NUM1_YEAST	RPM2_YEAST	DPOL_METJA	SPSA_BACSU
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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MEDLINE-95350630; PubMed-7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutron G., Fitzhugh W., Fields C.A., Gocayne J.D., Soctt J.D., Shirley R., Liu L. I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Gnehm C.L., Krichman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                296 ATNNNPSITSKGNISLDWRLEHFKKTDNLRLCDSPFRY---FVAGNVAFSKEWLNKVGWF 352
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Haemophilus.
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-- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative glycosyl transferase H11578 (EC 2.-.-).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        660 GINYYNYDKFDDLDESRK----YIFNKTAEYQEEMDMLKDLKLIQ----NKDAKIAVSIF 711
                                                                                                                                                                                                                                                                                                                                     433 PLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRI 492
                                                                                                                                                                                                                                                                                                                                                                                                                                125 IIVEKECGIIGSQYKTGDIWKNPLLHNDICEAMLFYNPIHNNTMIMRANVYREHKLIFNK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVNQSLNRQ 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223 --SVYNHEQNETAKKIKRENITYYLNKIG---IDIKVINSVSLLEIXHVDKSNKVLKSIL 277
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                          64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          712 YPNTLNGLVKKLNNIIEYNKNIFVIILHVDKNHLTP-DIK---KEILAFYHKHQVNIL 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    278 Y------EMYMSLDKYTITSLEHFIKYHLELFDLKQNLKIIKKFIRK-INVI 322
                                                                                                                                                                                                                                                                                                                                                                                                           493 MS-KPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDKTLACV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  547 YTTNRNVNPDGSLIANGYNWPE-FSREKLTTAMIAH---HFRMFTIRAWHLTDG---FNE
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STARAIN-KIZ / MGIG55;
MEDLINE=94316500; PubMed=8041620;
Sofia H.J., Burland V., Danlels D.L., Plunkett G. III, Blattner F
Sofia H.J., Burland V., Danlels D.L., Plunkett G. III, Blattner F
Analysis of the Escherichia coli genome. V. DNA sequence of the
region from 76 0. to 81.5 minutes.";
Nucleic Acids Res. 22:2576-2586(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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J. Biol. Chem. 264:5226-5232(1989).
-i- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 DYPYAEDYKFWSEVSRLGCLANYPEALVKYRLHGNQTS------
                                                                                                                                                                                                                                                                    DB 1; Length
                                                                                                                                                                                                                                                                                                     Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aronson B.D., Somerville R.L., Epperly B.R., Dekker E.E.
Aronson B.D., Somerville R.L., Epperly B.R., Dekker E.E.
"The primary structure of Escherichia coli L-threonine
                                                                                                                                                        Interpreto; IRO01173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                  323 AA; 37680 MW; 7CBC2681039AB5B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YIBD_ECOLI STANDARD; PRT; 344 AA.
P11290; P22999;
01-JUL-1989 (Rel. 11, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2091 (Rel. 40, Last annotation update)
Putative glycosyl transferase yibD (EC 2.-.-).
                                                                                                                                                                                                                                                                4.4%; Score 224.5; DB 1
ilarity 23.2%; Pred. No. 1.5e-05;
Conservative 65; Mismatches 145
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                                                                                                                            EMBL; U32832; AAC23227.1; -
                                                                                                                                                                                                                       Complete proteome. SEQUENCE 323 AA;
                                                                                                                                                                                                                                                                                        Local Similarity
nes 83; Conserv
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Freymond P., Karamata D.;
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P46918;
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         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                           MMNSTNKLSVIIPLYNAGDDFRTCME -> MRAMISALVWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 -NADWCFRETGETWOSIPTDRLRSTGVLTGPDWLRMGLSSRRWTHVVWMGVYRRDVIVKN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           648 HFVVVNQSLNRQGINYYNYDKFDDLDESRRYIFNKTAEYQ-----EEMDMLKDLKL 698
                                                                                                                                                                                                                                                                                                                                 435 VSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIMS 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=99350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
                                                                                                                                                                                                                                                                                                                                              495 KPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKD--KTLACVYTTNRN
                                                                                                                                                                                                                                                                                                                                                                                                                             553 VNPDGSLIANGYNWPEFSREKLTTA------MIAHHFRMFTIRAWHLTDGFNENIEN
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                                                                                                                                                                                                                                                                                                            65;
                                                                                                                                                                                                                                                                                     Length 344;
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                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                              EcoGene; EG11266; yibb.
Interpro; IRR01173; G1ycos_transf_2.
Pfam: PF0055; G1ycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
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9B5DABFE86D5457A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative glycosyl transferase H10868 (EC 2.-.-).
                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                           57; Mismatches 128;
                                                                                                                                                                                                                                                                                   4.3%; Score 217.5; DB 23.1%; Pred. No. 4e-05;
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                                                                                                                                                                                                                                                             40524 MW;
                                                                                                   EMBL; U00039; AAB18592.1; -.
EMBL; AE000439; AAC76639.1; -
EMBL; X06690; CAA29885.1; -.
PIR; A30258; Q3ECTH.
PIR; B33276; B33276.
                                                                                                                                                                                                                                                                                                          75; Conservative
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                                                                                                                                                                                                                                                             344 AA;
                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                              Complete proteome.
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                                                                                                                                                                                                                 "Whole-genome random sequencing and assembly of Haemophilus influenzae ^{\rm h} ".
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          611 LKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVNQSLNRQGINYYNYDKFD 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                671 DLDESRKYIFNKTAEYQEEMDMLKDLK--LIQNKDA------KIAVS----- 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------KHEDYAFFLDCLKEVKQSILYSHQASSFVRIGKVSVSSNKFKSAIWTFN 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          492 IMSKP-NGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDKTLACVYTTN 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -KLVTTSK-----KIDYLTLLQG-------NQFKIMTVLVERESIKLLRFPNI- 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D. Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.Fine L.D., Fritchman J.L., Geoghagen N.S. M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                               -! - SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 250;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro: IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250 AA; 28915 MW; A5D8220129782E98 CRC64;
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23.6%; Pred. No. 4.1e-05;
Lve 49; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Minor teicholc acids biosynthesis protein ggab.
GGAB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U32768; AAC22526.1; -.
HSSP; P39621; 1QGQ.
TIGR; HIO868; -.
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                                                                                                                                                                                                                                                                                          Science 269:496-512(1995).
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                                                                                                                                                                                    Venter J.C.;
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EMBL; AP003591; BAB74535.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=103690;
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                                                                                                                             234 HSL-----
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P22639;
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                                                                                                                 RA Kunster, observations, rudmeu-soball, and bentini A.M., Alloni G., Kunster, Ogasawatan N., Mosser I., Albertini A.M., Borchert S., Radedo V., Bestlero M.G., Bessleres P., Bolotin A., Borchert S., Raevedo V., Bertero M.G., Bessleres P., Bolotin A., Borchert S., Raevedo V., Bertero M.G., Brans A., Braun M., Brignell S.C., Bron S. Borniss R., Burnier I., Godani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Grian M.D., Errington J., Fabret C., Ferrari E., Poulger D., Ra Entian K.D., Errington J., Fabret C., Ferrari E., Poulger D., Ra Fitz C., Fujita M., Fujita Y., Fabret C., Ferrari E., Foulger D., Andreys M., Glaser P., Goffeau A., Golightly E.J., Grandi G., Ra Guiseppi G., Karamata D., Kasahara Y., Klaerr-Blanchard M., Moles L., Albosto S., Hullo M.F., Itaya M., Jones L., Aurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Kurita K., Lapidus A., Lardinois S., Lauber J., Noback M., Reynor D., O'Reilly M., Pournelle B., Rapoport G., Rey M., Reynolds S., Raecon E., Poil T.M., Portetelle D., Porwollik S., Prescott A.M., Reyeser M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Scanlan E., Schleich S., Schroeter R., Scoffone F., Scanlan E., Schleich S., Schroeter R., Scotlin B., Tarkant M., Tarmakoshi A., Tanamato H., Yanane K., Scotlon M., Tamakoshi A., Tanamate H., Wedler H., Wedler E., Wedler E., Wedler H., Wedler E., Walners P., Wasarotti A., Tanamato H., Yanane K., Yasumoto K., Yata K., Vasarottin Bacillus R., Voshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Wohlkaw H., Danchin A., Tanamato H., Yanane K., Wasarottin Bacillus R., Subhils S., Subhils M., Sanber D., Schrieber G., Ere S., Solotin M., Panamato G., Ere S., Solotin M., Walnetter Gram-positive bacterium Bacillus R., Subhils S., Subh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NATURE 390:249-256(1997).
-I- FUNCTION: INVOLVED IN THE BIOSYNTHESIS OF GALACTOSAMINE-CONTAINING MINOR TEICHOIC ACIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 PIFFAEGRIGEHNLN-----NKFS----STRILDVEKEPHHILTHCCSTFIKKDALKN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       597 --FNENIENAVDYDMF-LKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVN 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 436 SIYIPAYNCANYIQRCVDSALNQIV--VDLEVCICNDGSTDNTLEVINKLYG----NNPR 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 IVYAKKQNGGVSSARNYGLKYAEGRYIQFLDPDDLVSEGTFENVLNFFDEHKNEIDIVAI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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21.3%; Pred. No. 0.00025;
.ive 94; Mismatches 240; Indels 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1 - SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e; Glycosyl_ransferase; Complete proteome.
900 Aa; 107154 MW; FA66495488C2C62F CRC64;
(AUG-1994) to the EMBL/GenBank/DDBJ databases.
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InterPro; IrRO01173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Transferase; Glycosyltransferase; Com
                                                                                                            MEDLINE=98044033; PubMed=9384377;
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                                                                                                                                                                                                                                                                                          261 MVMHDLKWKLLIKDISETPLDENEYSEFLTLIREVLSYIDDDVIIE--TKSVSHFYLYHA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         378 LFNSKGFKFYAKIGETKIKAKNIKRQHNDYISLGEVIKKYPGFSIDIPKGHLADNHHIBF 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---QFALLILEKKTGH----------------VFNKTSTLTYMPWERKLQWTN 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   492 FIKEFRFLKSLHKSGEKSKKRKSALKKALMARWVHHVFTIFNRKPVWLFIDRODKADDNA 551
                                                                                           QSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQNKDAKIAVSIFYP 713
                                                                                                                                                                                                                                                                                                                                                                       813
-----ITFSKNL------IDIIKNHEQKIPLFLQY-
                                                                                                                                                                                                                                 714 NTLNGLVKKL------NNIIEYNKNIFVIILHVDKNHLTPDIKKEILAFYHKHQ
                                                                                                                                                                                                                                                                                                                                                                    762 VNILLNNDISYYTSNRLIKTEAHLSN----INKLSQLNLNCEYIIFDNHDSLFVKN----
                                                                                                                                                                                                                                                                                                                                                                                                              ------DSYAYMKKYDV-GMNFSALTHDWI---EKINAHPPFK-KLIKTYFNDN-DLRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MNVKGASQGM----FMKYA-LPHELLTIIKEVITSCQSIDSVPEYNTEDIWF----
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-i- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1991 (Rel. 19, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative glycosyl transferase alr2836 (EC 2.-.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   322 AA.
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Pfam; PF00535; Glycos_transf_2; 2.
Lipopolysaccharide biosynthesis.
SEQUENCE 1275 AA; 139596 WW; 3AF9662A10A140F1 CRC64;
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01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herrmann R.;
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P75086;
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                                                                                                                                                                                                                                                -KDKTLACVYTTNRNVNPD-GSLI----ANGYNWP-----EFSREKLTTAMIAHHFRMFTI 588
                                                                                                                                                                                                                                                                 -----KKLGIQKKNHFVVVNQSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQEE 689
                                                                                                                                                                                                                                                                                                                                                                 SATSEQEAKSQAGIEMTNQY--INDFLVRIGYG-----ARVDLSRNLQYRTKYYQRS 270
                                                                                                                                                435 VSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNP-RVRIM 493
                                                                                                                                                                      3 ISVIISNYNYARYLSRAINSVLAQTHSDIEIVIVDDGSTDNSRDVITQLQEQAPDKIKPI 62
                                                                                                                                                                                                                                                                                                  ----RAWHLTDGFNENIENAVDY-DMFLKLSEVGKFKHLNK-ICYNRVLHGDNTSI---
                                                                                                  Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; delta subdivision; Myxobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
                                                                                                                        Indels
            PIR; B35391; B55391.
InterPro; IRP01173; Glycos_transf_2.
Pfam; PF00555; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
                                                                         322 AA; 36388 MW; 753C2FB59327D968 CRC64;
                                                                                                                                                                                                SKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFL---
                                                                                              Match 3.9%; Score 199.5; DB 1; Local Similarity 26.4%; Pred. No. 0.00034; les 81; Conservative 48; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
0-antigen blosynthesis protein rfbC.
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InterPro; IPR001296; Glycoc_transf_l.
InterPro; IPR001173; Glycoc_transf_2.
Pfam: PF00534; Glycos_transf_l: 1.
 EMBL; AF031959; AAC32401.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-96198166; PubMed-8626291;
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                                                              Complete proteome. SEQUENCE 322 AA;
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                                                                                                  Query Match
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                                                                  14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GINYYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQNKDAKIAVSIFYPNTLNGL 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 720 VKKLNNIIEYNKNIFVIILHVDKNHLTPDIKKEILA--FYHKHQVNILLNND----- 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                570 -----VRGTPKVSIIVPFKDRPDLLRTLVDSLLAQTRYPHFEVLLVSNNSTRPETFAL 622
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                                                                                                                                    427 SHIHRIPLVSIYIPAYNCAN-YIQRCVDSALNQTVVDLEVCICNDGST-DNTLEVINKLY 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     433 ALLYTDEDGLDAQGHRSAPFFK-PDWSPDLLRSVDYVRHFLVVRRETLAQVGGLREGFDG 491
                                                                                                                                                                           313 ARLSRRPLISLVTPVHDASEAFLRECLASVSSQVYADWEWLLVDDASTAPHLARILREAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     485 GNNPRVRIM-SKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDKTL
                                                                                                                                                                                                                                                                                                                                    373 ERESRIRVLTASSEGDTARATNEGFAACRGDFVGFLGAEDTLSPHALAEVALAFLAQPEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           604 AVDYDMFLKLSE-VGKFKHLNKICYNRVLHGDNTSIKK---LGIQKKNHFVVVNQSLNRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               551 G-----TSPAPIOYRVRYP----
                                                                  71;
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NCBL_TaxID=2104;
Length 1275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2. STRONG, TO M.GENITALIUM MG025.
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                                                                  Indels
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Putative glycosyl transferase MG025 homolog (EC 2...-)
(801_orf299V).
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                                                                  71; Mismatches 176;
   DB 1;
Score 197.5; DB Pred. No. 0.0026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35, Created)
35, Last sequence update)
40, Last annotation update)
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InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
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MEDLINE-97105885; Pubmed-8948633;
3.9%;
                                                                     84; Conservative
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                                  Best Local Similarity
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EX5B_BUCAI
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AC P57529;
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A Kunst F., Ogaswara N., Moszer I., Albertini A.M., Alloni G.,
A Azevedo V., Bertero M.G., Bessleres P., Bolotin A., Borchert S.,
A Azevedo V., Bertero M.G., Bessleres P., Bolotin A., Borchert S.,
Borlise R., Boursier L., Brans A., Braun M., Brignell S.C., Brons S.,
A Borlise R., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
A Choi S.K., Codani J., Fabret C., Ferrari E., Foulger D.,
A Britan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
A Britan K.D., Errington A., Golightly E.J., Grandi G.,
A Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
A Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Henaut A.,
A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
A Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Mediua C.,
A Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
A Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
A Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
                                                                                  10;
                                                                                                                                                                                                                                                 --YISPKRRRFLKPYFGKTGVIEQKTKLRTPHSQPLAKFYRHEIFHLLDPLKEKL---FY 179
                                                                                                                                                                                                                                                                               661
                                                                                                                                                                                                                                                                                                         217
                                                                                                                                                                                                                     550 NRNVNPDGSLIANGYNWPEFSREKLTTAMIAHH---FRMFTIRAWHLTDGFNENIENAVD 606
                                                                                                                                                                                                                                                                                                                                                              F----GAGIVIYIY---TMLPGFLK 254
                                                                                                                                                                                           66 YLEKPNGNWGSVVNFVKQNQLAKGOYITVLDSDDYFLANAFORVAAHFGHDMIVSAFYC- 124
                                                                                                            434 LVSIYIPAYNCANYIQRCVDSAL - - NQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVR 491
                                                                                   Gaps
                                                                                                                              607 YDMFLKLSEVGKFKHLNKIC----YNRVLHGDNTSIKKLGIQKKNHFVVVNQSLNRQGI
                                                                                                                                                                                                                                                                                                                                   (FDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQNKDAKIAVSIFYPNTLNGLVK
                                                                                                                                                                  492 IMSKPNGGIASASNAAV--SFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDKTLACVYTT
                                                         DB 1; Length 299;
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Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus NCBI_TaxID=1423;
Hypothetical protein; Transferase; Glycosyltransferase; Complete proteome. SEQUENCE 299 AA; 34935 MW; 9A3AF2F099283565 CRC64;
                                                                                                                                                                                                                                                                                                180 QDCLLTHNAINKVQSVFYICEPLAVWYATRPGNSTTMP------
                                                       3.8%; Score 193.5; DB 1;
24.5%; Pred. No. 0.00066;
iive 38; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Minor telchoic acids biosynthesis protein ggaA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            446 AA
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f01-NOV-1995 (Rel. 32, Last seques J5-JUN-2002 (Rel. 41, Last anno
                                                                       Local Similaricy and 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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SEQUENCE FROM N.A.
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                                                                      Similarity
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P46917;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 390:249-256(1997).
-!- FUNCITON: INVOLVED IN THE BIOSYNTHESIS OF GALACTOSAMINE-CONTAINING
-!- FUNCITON: LONGLOED IN THE GLYCOSYLTRANSFERASE FAMILY 2.
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
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Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Satolian E., Schletch S., Schroeter R., Scoffone F., Sekjuchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takamaru K., Sorokin A., Tanakoshi A., Tanakashi H., Tarepstra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Waitzeneger T., Viari A., Wanhat A., Zumaren K., Yamanoc K., Yasumoto K., Yata K., Yoshikawa H.F., Zumarein E., Yoshikawa H. Z., Zumarein E., Zumarei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----FNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVV 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------EGKYFYRK----RKEQDSLVDRSWFNKKRYTYLLNECY 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          434 LVSIYIPAYNCANYIQRCVDSALNQTV---VDLEVCICNDGSTDNT---LEVINKLYGNN 487
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Subtilist; BG11367; ggaA.
InterPro; IPR001173; G1vos_transf_2.
Pfam; PF00535; G1ycos_transf_2; 1.
Transferase; G1ycosyltransferase; Complete proteome.
SEQUENCE 446 AA; 53148 MW; BB3698D9B6856C42 CRC64;
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342 TSAKIKGLRLELTGHFINQYYEMKENDRIYIK-----YFKR 377
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21.5%; Pred. No. 0.0014;
1ve 69; Mismatches 136;
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les 99; Conservative
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P57529;
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949 GKKTGLMIHYILKNLHVLKNKNSNWFSCILEKYNIHIK---WTSVLIYWIKNIINTPLND 1005
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STRAIN-ATCC 35210 / B31;
STRAIN-ATCC 35210 / B31;
MEDLINE-98065943; PubMed-9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weldman J.,
Utterback T., Watthey L., McDonald L., Artlach P., Bowman C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1006 EKIILSRIDEKSSIRELEFFFPIKNMLYSTELNKIIQSINPTSITSPQLSFNPVKGMLTG 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1066 FVDLVFIWKKKYYILDYKSNWLGKNNNFYSSIHINKEIVKKRYHLQYQ------IYTI 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----CEYIIFDNHDSLFVKNDSY-----AYMKKYDVGMNFSALTHDWIEKI 839
                                                                                                                                                                                                                                                                                                                                                                               630 --VLHGDNT-----SIKKLGIQKKNHFVVV---------NQSLNR 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                838 GFTIQGGKTMNYEGLLEKLKKLSI---NNFIEVKNNTDNFSFSRKPQTISLICKNKFLNK 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGI-NYYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQNKDAK----IAVSIFYP 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           895 KNIRNTWSITSFSQLNK----INKLSKHHQKEVALKEL-CIKNQEKKNQSLLTIHNFPK 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 714 NTLNGL-----VKKLNNIIEYNKNIFVIILHVDKNHLTPDIKKEILAFYHKHQVNILLNN 768
                                                                                                                                                                                                                     678 ENHIKNLNFLHIGELLQEQFQFFKKISLIRWFQKKISTKTQPEYNESIKCFDESPSIKI 737
                                                                                                                                                                                                                                                                                                                                                     547 YTTNRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWH----LTDGFNENIE 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         840 NAHPPFKKLIKTYFNDND-----LRSMNVKGASQGMFMKYALPHELLTIIKEVIT 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                       --PISFFLQEEKEVSIDDYQVWISK--QCANEI
                                          357 NHWGGEDVEFGYRLFAKGCFFRVIDGGMAIHQEPPGKENETEREAGKSITLKIVKEKVPY
                                                                            ----LTCAKTGKAKITTKNGEKILTANDIAILVR-
                                                                                                                     417 IYRKLLPIEDSHIHRIPLVSIYIPAYNC-----ANYIQRCVDSAL---NQTVVD----
                                                                                                                                                         559 -NRKEADLIQDELEKLNIISIYSSNKNSVFQTLDAQELLWILESILEPENEILLQQSMAS
                                                                                                                                                                                               ----- LEVCICUDG-STDNTLEVINKLY------GNNPRVRIM---SKPNGGIASAS
                                                                                                                                                                                                                                                                          505 NAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLK-------DKTLAC-----V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Exodeoxyribonuclease V beta chain (EC 3.1.11.5).
RCB OR BB0633.
    476 PVVPSSKNLKMNFTINDVAQT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53;
                                                                                                                                                                                                                             pfam; PF00580; UvrD-helicase; 1.
Hydrolase; Nuclease; Exonuclease; Endonuclease; Helicase; ATF-binding;
DNA repair; Complete proteome.
NP_BIND 25 32 ATF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 SILKYFTKRNIEKNTINNTCSKYIIFEESEKILKKKFSL-----KNVIIIYAVKKIHQF 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 PSITSKGNISLDWRLEHFKKTDNLRLCDSPFRYFVAGNVAFS----KEWLNKVGWFDEEF 356
                                                                                                Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 SNVKKLTLSESEKNSLKNKW-KSITGKKSENAEIRKVELVPKDFPKDLVLAPLPDHVNDF 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 KENLLTIVQKYEQKLDIKYVRQKDYGYQLCAVRNLGLRTAKYDFVSILDCDMAPQQLWVH 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        383 DEFQDTDIQQY-KIFNLLYKKNKTTVLFL-----IGDPKQAIYSFRGAD-----IF 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYLTELLEDNDIVLIGPRKYVDTH------NITAEQFLNDPYLIESLPETATNNN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NDYELALKLFEKSAETYGRKIVEFQIIKCKEKLSTNSYVSEDKKNSVCDSSLDIATQLLL 73
                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: Exonucleolytic cleavage (in the presence of ATP) in either 5' to 3'-or 3'- to 5'-direction to yield 5'-phosphooligonucleotides.
SUBUNIT: CONSIST OF THREE SUBUNITS; RECB, RECC AND RECD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250 NDLEINKKIYSK-----FNLIKWINK----ITEWAKSETKDYIP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340 LLKEKKKKSL----IGFNDLLSILLKTIKKEKFLKDLII-----KKYPAAFI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 TWYKNRKKSLGIKPVNKNIGLSIIIPTFNRSRIL-DITLACLVNQKTNYPFEVVVADDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.7%; Score 189; DB 1; Length 1174; Best Local Similarity 18.6%; Pred. No. 0.0067; Matches 200; Conservative 172; Mismatches 348; Indels 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           342 347 POLY-LYS.
1174 AA; 139037 MW; 668FE1336F1F190A CRC64;
                                                                                                                   symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
NCBI_TaxID=118099;
16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Exodeoxyribonuclease V beta chain (EC 3.1.11.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .nterPro; IPR000212; UvrD-helicase.
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                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-TOkyo 1998;
                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY)
                                                                              RECB OR BU454.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44;
                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGERAMS; TIGRO0609; recB; 1.
Hydrolase; Nuclease; Exonuclease; Endonuclease; Helicase; ATP-binding;
DNA repair; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YIIKCLDRKQSFKTLNYILSSKILNVPWNLQRILIKQDKICLIEEFIENIIVLLEKNEIT 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          390 PPGKENETEREAGKSITLKIVKEKVPYIYRKLLPIEDSHIHRIPLVSIYIPAYNCANYIQ 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----IYHKEQNIQSLIS 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       423 TDARIVLKINHRSSKKLIG--PLNKIFNNIYNNAIADEIEK---IDFTNS-LPNCKNDNN 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----GNVAFSKEWLNKVGWF--DEEFNHWGGEDVEFGYRLFAKGCFFRVIDGGMAIHQE 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 WKSITGKKSENAEIRKVEL--VPKDFPKDLVLAPLPDHV-----NDFTWY----KNR-- 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :| | :::: ::| | |: | | 363 YKIILIDEAQDLSLIQIEIFKILKTAGIKLIFIADPRQIIYSFRKADISFYNKEIKNKIN 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----KKSLGIKPVNK---NIGLSIIIPTFNRSRILDITLACLVNQKTNYP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | : : | : : | : | 477 KIVINGQEIEGINITTUTESEEDINQKTALTIKYLLA-YGK---IAENNKIRNIKMQD 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 VEFQIIKCKEKLSTNSYVSEDKKNSVCDSSLDIATQLLLSNVKKLTLSESEK--NSLKNK 92
                                                               FUNCTION: REQUIRED FOR EFFICIENT DNA REPAIR; IT CATALYZES THE UNWINDING OF DOUBLE-STRANDED DNA AND THE CLEAVAGE OF SINGLE-STRANDED DNA AND IT STIMULATES LOCAL GENETIC RECOMBINATION.

ALL OF THESE ACTIVITIES REQUIRE CONCOMITANT HYDROLYSIS OF ATP (BY SIMILARITY).

CATALITIC ACTIVITY: Exonucleolytic cleavage (in the presence of ATP) in either 5' to 3' or 3' to 5' direction to yield 5' phosphooligonucleotides.

SUBUNIT: CONSIST OF THREE SUBUNITS; RECE AND RECD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          634 LINAINKITFEKNLMIKIANITKDQKIIEWAKNKINY-----KGLLI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 FEVVVADDGSKENLLTIVQKYEQ-----KLDIKYVRQKDYGYQLCAVRNLGLRTAKYDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IKVL-------CRGKNEINLIDKALKKEQIQT-NKTQEKFLKTKEFSEIF
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Roberts K., Hatch B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.6%; Score 183; DB 1; Length 1169;
llarity 19.3%; Pred. No. 0.014;
Conservative 138; Mismatches 321; Indels 272;
                                                                                                                                                                                                       (BY SIMILARITY).
SIMILARITY: BELONGS TO THE HELICASE FAMILY. UVRD SUBFAMILY.
                         sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP (POTENTIAL).
IW; B61D63C1C959B91F CRC64;
Horst K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR004586; RecB.
InterPro; IPR000212; UvrD-helicase.
 Cotton M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00580; UvrD-helicase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137828 MW;
                                                                                                                                                                                                                                                                                                                                                             EMBL; AE001164; AAC66981.1; -.
                                             burgdorferi.";
Nature 390:580-586(1997).
   ., Fujii C., Co.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 1169 AA;
                                                                                                                                                                                                                                                                                                                                                                            P56255; 1PJR.
BB0633; -.
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Matches 175; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----KFDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQNK---DAKIAVSIFYPNTLNGLV 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKLNN---IIEYNKNIFVIILHVDKN-----HLTPDIKKEILAFYHKHQV----NILL 766
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RCVDSALNQTVVDLEVCICNDGSTDNTLEVI----NKLYGNNPRVRIMSKP--NGGIASA
                                             TLESLIINEEPPEIEEKINNINNDNESIELMTIHKSKGLGMNIVFLLNTTPIENSNFFSK
                                                                                                                                    826 ITSKLLEIAKIFTIDDIKHDFNIHEFIGQKRFNKKKYNTNVNTKLIPPKPIIKNMFK-KE
                                                                                                                                                                                                                                                                                                                     FSREKLTTAMIAHHFRMFTIRAWHLTDGFNENIENAVDYDMFL-----KLSEVGKFKH--
                                                                                                                                                                                                                                                                                                                                                                          YTSSFSSLTAQAHHKEFYENYDF---KNINYEKETELDYEPGLEETLPKGKDIGNILHAA
                                                                                                                                                                                                                                                                                                                                                                                                                                622 LNKICYNRV-----LHGDNTSIKKLGIQKKN---HFVVVNQSLNRQGINYXNYD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa "Genome sequence of the endocellular bacterial symbiont of Buchnera sp. APS.";
Nature 407:81-86(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                        SNAAVSFAKGYYIGQLDSDDY-LEPDAVELCLKEFLKDKTLACVYTT----
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TRANSMEM 12 32 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.5%; Score 177.5; DB 1; Best Local Similarity 20.3%; Pred. No. 0.022; Matches 202; Conservative 134; Mismatches 302;
                                                                                                                                                                                                                     -- NRNVN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
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MEDLINE-20445173; PubMed-10993077;
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P57189;
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Qy Db	Qy 67 IATQLLLSNVKKLTLSESEKNSLKNKWKSITGKKSENAEIRKVELVPKDFFKDLVLAPLP 126 : : :: : : : Db 96 IETKNVILSLKKNTASNFSQNSLPSKISKNIFFIKYPIILKKIHADKIL 144		
Qy Db	QY 127 DHVNDFTWYKNRKKSLGIKPVNKNIGLSIIIPTENRSRILDITLACLVNQKTNYPF 182		
č q	183 EVVVADDGSKENLLTIVQKYEQKLDIKYVRQKDY 		
9. Pb	232		
op G	QY 280 EQFLNDPYLIESLPETATNNNPSITSKGNISLDMRLEHFKKTDN 323 1 33 580 KVIFNNDYSISCVMNSKTVIPSLYNKSINFQLKANFNVDHQL-IFKLISKDLYNMKINGL 338		
oy Ob	QY 324LRLCDSPFRYFVAGNVAFSKEWLNKVGWFDEEFNHWGGEDVEFGYRLFAKGCF 376		
O O	377		
oy Og	QY 427SHIHRIPLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVC 466		
oy Ob	QY 467 ICNDGSTDNTLEVINKLYGNNPRVRIMSKPNGGIASASNAAVSFAKGYY 515 Db 479		
O.y	Qy 516 IGQLDSDDYLEPDAVELCLKREFLKDKTLACVYTTNRNVNPDGSLIANGYNWPEFSR 571		
Oy Dp	OY 572 EKLTTAMIAHHFRMFTIRAWHLTDGFNENIENAVDYDMFLKLSEVG 617		
S S	Qy 618 KFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVNQSLNRQGINYYNY 666		
o o o	QY 667 DKFDDLDESRKY 1FNKT-AEYQEEMDMLKDLKLIQNK 702 		
o, do	OY 703 -DAKIAVSIFYPNTLNGLVKKLNNIIEYNKNIFVIILHVDK 742 1		
O.Y	743		
Oy Dp	QY 783 AHLSNI		
Oy Dp	Qy 816YAYMKKYDVGMNFSALTHDWIEKINAHPPFKK 847 		

298 AA.

PRT;

STANDARD;

Y025_MYCGE P47271; Q49359;

RESULT 13 Y025_MYCGE ID Y025_MY

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STRAIN—FATCC 33530 / G-37;
STRAIN—96026346; PubMed=7569993;
Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
The minimal gene complement of Mycoplasma genitalium."; 548 66 YFEKTNGNWGSVINYVKKNKLALGQYITVLDSDDYFLKDSFKKVARFFGHDMIIGAFYCY 125 712 549 TNRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGFNENIENAVDYD 608 609 MFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVNQSLNRQGINYYNYDK 668 434 LVSIYIPAYNCANYIQRCVDSAL--NQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVR 491 Gaps 492 IMSKPNGGIASASNAAV--SFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDKTLACVYT-669 FDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQNKDAKIAVSIFY------ch 3.5%; Score 176.5; DB 1; Length 298; 1 Similarity 21.8%; Pred. No. 0.0055; 80; Conservative 40; Mismatches 118; Indels 129; Mycoplasma genitalium. Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma NCBI_TaxID=2097; SEQUENCE OF 172-298 FROM N.A.
STRAIN-ARCC 33530 / G-37;
MEDLINE-940/5230; PubMed-8253680;
PEterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
"A survey of the Mycoplasma genitalium genome by using random 4 sequencing."; J. Bacteriol. 175:7918-7930(1993). -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY STRONG, TO M.PNEUMONIAE MPN028. InterPro; IPR001173; Glycos_transf_2. Pfam; PF00535; Glycos_transf_2; 1. Hypothetical protein; Transferase; Glycosyltransferase; 200 201 EP -> DA (IN REF. 2). 298 AA; 35044 MW; B7BCCC73EB2CA023 CRC64; 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative glycosyl transferase MG025 (EC 2.-.-). EMBL; U39682; AAC71241.1; -. EMBL; U02253; AAD12517.1; -. Local Similarity Complete proteome. SEQUENCE Query Match Best Loca Matches g a 셤 δ ŏ g ò ò

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EXEN_CLOBU STANDARD;
Q06366;
01-FEB-1995 (Rel. 31, Created)
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ID BXEN_C
AC Q06366
DT 01-FEB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i - CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
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-----PNTLNGLVKKLNNIIEYNKNIFVIILHVDKNHLTPDIKKEILAFYHKHQVNIL 765
                          214 TITSWENPNKFNAWCEILQKMNLYGAGIVIYIY-----TMLPGFLKQL----KKKQLILN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                + {DNA}(N).
--- SUBCELULAR LOCATION: Cytoplasmic (By similarity).
--- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-C FAMILY. POLC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                    E.Y.,
                                                                                                                                                                                                                                                 Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
NCBI_TaxID=134821;
                                                                                                                                                                                                                                                                                                                                                                                                        Nature 10757-762(2000).
Nature for required for replicative dna Synthesis. THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.5%; Score 176; DB 1; Length 1442;
llarity 17.9%; Pred. No. 0.045;
Conservative 176; Mismatches 378; Indels 38
                                                                                                                                                                                                                                                                                                                                                 Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen Cassell G.H.;
                                                                                                                                                                                                                                                                                                                                                                             complete sequence of the mucosal pathogen Ureaplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transferase; DNN-directed DNA polymerase; DNA replication Nuclease; Exonuclease; Complete proteome.

DOMAIN 409 575 EXONUCLEASE.

SEQUENCE 1442 AA, 166227 MW; 834C3EF722ACA6D1 CRC64;
                                                                                                                                                                                 16-Ocr-2001 (Rel. 40, Created)
16-Ocr-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA polymerase III polC-type (EC 2.7.7.7) (PolIII).
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InterPro; IPR000520; Exonuclease.
InterPro; IPR003141; PHP_N.
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                                                                                                                                                         STANDARD;
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LNHKPAY 271
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| | | | | | | | 334
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                                                                                                                                                KYVRQKDYGY-----QLCAVRNLGLR---TAKYDF----VSILDCDMAPQQLWVHSY
                                                                                                                                                                                                                                   LTELLEDNDIVLIGPRKYVDTHNITAEQFLNDPYLIESLPETATNNNPSITSKGNISLDW
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ----IIEFGAVIMONN-------KOIGEKIOFFIKPIOQIN
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                                                                  LDITLACLVNQKTNYPFEVVVADDGSKENLLT---
      --NCEYI-
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1162 AA.

PRT;

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                                                                                                                                                                                                                   nontoxic
                                                     Clostridium butyricum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                Fujii N., Kimura K., Yokosawa N., Oguma K., Yashiki T., Takeshi K., Ohyama T., Isogai E., Isogai H.; Simiarity in nucleotide sequence of the gene encoding nontoxic component of botulinum toxin produced by toxigenic Clostridium butyricum strain BL6340 and Clostridium botulinum type E strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      375;
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llarity 19.5%; Pred. No. 0.036;
Conservative 137; Mismatches 322;
Ol-rEB-1995 (Rel. 31, Last sequence update) 01-NOV-1995 (Rel. 32, Last annotation update) Botulinum neurotoxin type E, nontoxic component. Clostridium butyricum
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Pfam; PF01742; Peptidase_M27; 1.
PRINTS; PR00766; BONTOXILYSIN.
ProDom; PD001963; Bontoxilysin; 1.
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MEDLINE-93360835; PubMed-8355622;
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Matches 202; Conserv
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Bacteria; proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
NCBI_TaxID=747;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
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                          May B.J., Zhang Q., Li L.L., Paustlan M.L., Whittam "Complete genomic sequence of Pasteurella multocida Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
EMBL, AE006116; AAK02859.1; -
                                                                                                  11 protein, Complete proteome.
965 AA: 111600 MW; 9C4B2CF80E1A6BD7
                                                                                                                               94.4%; Score 4802; DB 16;
llarity 93.0%; Pred. No. 6e-241;
Conservative 42; Mismatches 26;
                                                                    HSSP; P39621; 10GO.
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 2.
Hypothetical protein; Complete proteor
         STRAIN=PM70;
MEDLINE=21145866; PubMed=11248100;
                                                                                                                                             Similarity
FROM N.A.
                                                                                                                                                Local Simines 897;
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SEQUENCE
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                                                                              NKLYGNNPRVRIMSKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKD
                                                                                                   541 KTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGFNEN
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MEDILINE-98442423; PubMed-9770287;
MCDILINE-74, Zhang Y., Adler B.;
"The capsule blosynthetic locus of Pasteurella multocida FEMS Microbiol. Lett. 166:289-296(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chung J.Y., Zhang Y., Adler B.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
EMBL, AF067175; AAC67250.2; -.
HSSP; P39621; 10GQ.
InterPro; IRR01173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2.
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085457; OB5457;
01-NOV-1998 (TrEMBLrel. 0
01-CCT-2000 (TrEMBLrel. 1
01-UON-2002 (TrEMBLrel. 2
Glycosyl transferase.
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                     NTEDIWFOFALLILEKKTGHVFNKTSTLTYMPWERKLOWTNEQIOSAKKGENIPVNKFII
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  AHPPFKKLIKTYFNDNDLRSMNVKGASQGMFMKYALPHELLTIIKEVITSCQSIDSVPEY
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Pasteurella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Townsend K.M., Boyce J.D., Chung J.Y., Frost A.J., Adler B.; "Genetic Organization of Pasteurella multocida cap Loci and Development of a Multiplex Capsular PCR Typing System."; J. Clin. Microbiol. 39:924-929(2001).
EMBL; ARYO2467; ARXI7921.1; -...
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Last annotation update)
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Pfam; PF00535; Glycos_transf_2; 2.
Transferase.
SEQUENCE 965 AA; 111562 MW. FARDER
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MEDLINE-21142635; PubMed-11230405;
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                                           MNTLSQAIKAYNSNDYELALKLFEKSAETYGRKIVEFQIIKCKEKL----STNS
ed. No. 5.9e-225;
Mismatches 60;
    Pred.
   86.88;
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STRAINS-P-1059, AND ATCC 15742;
MEDLINE-98192645; PubMed-9555958;
DeAngelis P.L., Jing W., Drake R.R., Achyuthan A.M.;
Identification and modecular cloning of a unique hyaluronan synthase
from Pasteurella multocida...;
J. Biol. Chem. 273:8454-8458(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ETATININPSITSKGNISLDWRLEHFKKTDNLRLCDSPFRYFVAGNVAFSKEWLNKVGWFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        972;
                                                                                                                                                                                                                                                                                                                                       Fuller T.E., Kennedy M.J., Lowery D.E.;
Fuller T.E., Kennedy M.J., Lowery D.E.;
Identification of Pasteurella multocida virulence genes in a ridentification of Pasteurella multocida virulence genes in a septicemic mouse model using signature-tagged mutagenesis.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF036004; AAC38018.1; -.
EMBL, AF237926; AAF68412.1; -.
HSSP, P39621, 1QGO.
Interpro; IPR001173; Glycos_transf_2.
Pfam; PR00555; Glycos_transf_2. 2.
SEQUENCE 972 AA; 111838 MW; 7D65D024C41ED362 CRC64;
                                                                                                             Pasteurella multocida.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
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                             Created)
Last sequence update)
Last annotation update)
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86.6%; Pred. No. 1.4e-224;
tive 63; Mismatches 60;
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PRT;
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                                    ovo-1998 (TrEMBLrel. 0
01-0UN-2002 (TrEMBLrel. 2
Hyaluronan synthase.
Pastouro.
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hes 842; Conservative
                           01-AUG-1998 (TrEMBLrel. 01-AUG-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                   NCBI_TaxID=747;
                                                                                                                                                  Pasteurella
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386 K-DKIEIQLKFMEENNF-IFSHTSYHKINE-------KGKYIESVHSGLF 426
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chercunani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
"Comparative genomics of Listeria species.",
                            118 NKLDNKDTIIYGGYELIDEKGNSLRYIKPDSVLPINKLN---ISLLPLLRGLIHGCSLLM
                                                                                                                                        234 ECNVLWSSFLHELTEEEMIKMEGSPYL-----FLTRTATFLSNNT-PYKKACDLANTWA
                                                                                                                                                                                LIQNKDAKIAVSIFYPNTLNGLVKKLNNI-IEYNKNIFVIILH----VDKNHLTPDIKKE
 LKEFLKDKTLACVY - - - - - TTNRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMF
                                                            587 TIRAWHLTDGFNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKK
                                                                                         PAKYFHEVGIFNEALPTTQDYDLWFKIFRVAPIHFDESILIKSRFHSEQGS-KKISNHNE
                                                                                                                       547 N------HFVVVNQSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLK
                                                                                                                                                                                                                                             753 -ILAFYHKHQVNILLNNDISYYTSNRLIKTEAHLSNINKLSQLNLNCEYIIFDNHDSLFV
                                                                                                                                                                                                                                                                                                        KNDSYAYMKKYDVGMNFSALTHDWIEKINAHPPFKKLIKTYFNDNDLRSMNVKGASQGMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Listeria monocytogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Listeriaceae; Listeria.
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EMBL, AL591977, CAC99168.1; -.
ListList; Lamo1090; -.
InterPro; IPR001173; Glycos_transf_2.
Pfam, PF00555; Glycos_transf_2.
Hypothetical protein; Complete proteome.
SEQUENCE 327 AA; 37843 MW; F7480656043EC2FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein lmo1090.
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SEQUENCE FROM N.A.
STRAIN-EGD-E / SEROVAR 1/2A;
MEDLINE-21537279; Pubmed-11679669;
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EMBL, AR003609; AAL02991.; -.
InterPro; IPR001173; Glycos_transf_2.
Pfam, PR00355; Glycos_transf_2.
Fransferase: Hypothetical protein; Complete proteome.
SEQUENCE 604 AA; 69121 MW; 514CDD81C3FB3AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barbe V.,
                 TDGFNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVN
                                                                                                                       QSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQNKDAKIAVSIFYP
                                                                                                                                                                                                                                           TSNRLIKTEAHLSNINKLSQLNLNCEYIIFDNHDSLFVKNDSYAYMKKYDVGMNFSALTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21442074; PubMed-11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe
Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
Raoult D.;
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBL_TaxID=781;
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24.8%; Pred. No. 1.3e-07;
tive 71; Mismatches 213;
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01-DEC-2001 (TrEMBLEel. 19, Last sequenc
01-MAR-2002 (TrEMBLEel. 20, Last annotat
Putative two-domain glycosyltransferase.
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Matches 124; Conservative
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STRAIN-MALISH 7;
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PLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRI 492 Gaps 3 PLVSVIIPVYNVEKYVKRCLDSVLEQTYHNLEVIVVNDGATDNSAKVIKSISDN--RIRY 81; Length 44; Mismatches 133; Indels DB 16; 5.7%; Score 292.5; DB 1 27.5%; Pred. No. 7.7e-08; a

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                                                                                                                                                                                                                                                                                                                                                       HFVVVNQSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDL---KLIQNKDA 704
                               -----NENIENAVDY----DMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKN 647
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May B.J., Zhang O., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

EMBL, ARO06155; ARM03224.1: -
Interpro, IPR001173; Glycos_transf_2.
Pfam, Pr00555; Glycos_transf_2.

Ppam, Pr00555; Glycos_transf_2.

Ppam, Pr00555; Glycos_transf_2.

ERQUENCE 337 AA, 39267 MW; 8639BGFB5F700DB4 CRC64;
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193 MSKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDKTLACVYTTNRN
                                                                                                                 VNPDGS-----LIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGF---
                                                                                                                                                       KIAVSIFYPNTLNGLVKKLNNIIEYNKNIFVIILHVDKNHLTPDIKKEILAFYHKH 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pasteurella multocida.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
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01-JUN-2001 (TIEMBLEEL. 17, Last sequence update)
01-DEC-2001 (TIEMBLEEL. 19, Last annotation update)
Hypothetical protein PM1140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 292; DB 16; 1; Pred. No. 8.5e-08; 67; Mismatches 124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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Matches
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Q9CLR9
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266 YSIYY-----FELCIKFNKTEXL------FSQNEKNIL- 292
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                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                             campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
NCBI_TaxID=197;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  607 YDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKK-----NHFVVVNQSLNRQG
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--SYFNKKQ 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 350;
                                                                                                                                                                                                                                                                                                Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF343914; AAK12955.1; ... InterPro; IPR001173; Glycos_transf_2. Pfam; PF00535; Glycos_transf_2? 1. Hypothetical protein. SEQUENCE 350 AA; 41616 MM; FB19017F89326E9E CRC64;
                                                                                                                                                                                                                                         STRAIN=NCTC 11828;
Oldfield N.J., Millar L.A., Ketley J.M.;
"Gene content polymorphisms in Campylobacter jejuni LOS
clusters.":
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                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical 41.6 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                               5.6%; Score 287.5; DB 2;
25.5%; Pred. No. 1.5e-07;
tive 66; Mismatches 129;
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  284 IKRILYDCYLSLVDNKLINILYFLR-
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Best Local Similarity 25.59
Matches 105; Conservative
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01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Pfam; PF00535; Glycos_transf_2;
PRINTS; PR00030; HTHCRO.
Transferase.
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80401 MW;
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                                              706 AA;
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01-MAR-2002
                                   NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                             495 KPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDKTLACVYTTNRNVN 554
                                                                                                                                                                                                                                                                                                         64 KENGGLSSARNTGIINAKGEYIYFLDSDDYIEYDSMKICYEIATKNKLDIVSFDAESFYD 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 -RYIIEDKIINDIK--SKKD-------IKSFKLDLQYR---FPLIIYTIKK 321
                                                                                                                                                                                                                                              VSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIMS 494
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                            Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       088090;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Putative glycosyl transferase (Fragment).
Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                     579 -IAHHFRMFTIRAWHLTDGFNENIENAVDYDMFLK------LSEVGKFKHLNKIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-OGIRF;
MEDLINE-98380380; PubMed-9712783;
Xu I., Murray B.E., Weinstock G.M.;
"A dluster of genes involved in polysaccharide biosynthesis from
                                                                                                                                                                                                                       93;
                                                                                                                                                                                                  Length 326;
                                                                                                                                                                                                5.5%; Score 279.5; DB 16; Length
25.2%; Pred. No. 3.6e-07;
tive 66; Mismatches 114; Indels
                                                                                                                                                                           326 AA; 38553 MW; 76503BF0B5DE1C03 CRC64;
                                                                                                                                                                                                                                                                                                                                         555 P-----DGSLIANGYNWPEFSREKLTTAM----
                                                                                                                  U.S.A. 99:996-1001(2002)
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 Clostridiales; Clostridiaceae; Clostridium
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                                                                                                   flesh-eater...
Proc. Natl. Acad. Sci. U.S.A. 99:996-100
EMBL; AP003187; BAB80207.1; -
Interpro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Complete protecome.
SEQUENCE 326 AA; 38553 MW; 76503BF0]
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Infect. Immun. 66:4113-4333(1998).
EMBL, AF071005; AAC35930.1; -.
InterPro; IPR001173; Glycos_transf_2.
InterPro; IPR000655; HTH_Cro.
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                                                                                                                                                                                                              Local Similarity
                                              TYPE A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                   SEQUENCE FROM N.A.
            NCBI_TaxID=1502;
                                                          PubMed-11792842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1351;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322 YLKKD 326
                                                                                                                                                                                                                       92;
                                              STRAIN-13
                                                                                                                                                                                                  Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               530 VELCLKEFLKDKTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIR 589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                DEEFNHWGGEDVEFGYRLFAKGCFFRVIDGGMAIHQEPPGKENETEREAGKSITLKIVKE 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKVTRLW-----IKAKKGFKYMAKNGIS-HTIQRAKIEKLRNQA--SYPNWLARN 161
                                                                                                                                                                                                                                                                                                                ------LEHFKKTDNLRLCDSPFRYFVAGNVAFSKEWLNK-----VGWF 352
                                                                                                                                                                                                                                                                                                                                                                              60 NOIYQTEPAIEAGFVVTLEGIKQKKVL----PFHFQSSAHVVTVDFPLNKKYPVIPGTE 114
                                                                                                                            Gaps
                                                                                                                                                                                                                              2 NEDIKVIFDSIYRDKTINNLTITGWALDTITKES--PTFTINNENQVSAYNIQRVLREDV 59
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Bacteria: Firmicutes; Bacillus/Clostridium group; Lactobacillales; Streptococcaceae; Streptococcaceae; Streptococcaceae; NCBL_TaxID=1313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 FYEVVKVLNENPELDLIYSDEDKIDMDGNRSDPAFK-PDWSPDLELGTNYISHLGVYRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        537 ENWLTLMVSFAQQERIGCVGAKLLYPNNTVQHAGVILGLGGVAGHGHYGYPHGDLGYFGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STD-NTLEVINKLYGNNPRVRIM-SKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          590 AWHLTDGFNENIENAVDYDMFLKLSE---VGKFKHLNKICYNRVLHGDNTSIKK--LGIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKNHFVVVNQSLNRQGINYYN-----YDKFDDLDESRKYIFNKTAEYQEEMDMLKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLIONKDAKIAVSIFYPNTLNG---LVKKLNNIIEYNKNIFVIILHVDKNHLTPDIKKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       754 LAFYHKHQVNILLNN-DISYYTSNRLIKTEAHLSNINKLSQLNLNCEYIIFDNHDSLFVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  488 AEFEQOLPGRFFVESIDIPF-----NFSTINNRAAKKAHGEYLLFLNNDTEVIT
                                                                                                                            Indels 167;
                                                                                                                                                                                          260 DNDIVLIGPRKYVD--THNITAEQFLNDPYLIESLPETATNNNPSITSKGNISLDWR-
                                                              DB 2; Length 706;
8710AD60C7D36315 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Glycosyl transferase, family 2/9lycosyl transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         822 YDVGMNFSALTHDWI----EKINAHPPFKKLIKTYFNDNDL 858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2001 (TrEMBLrel. 18, Created)
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                                               Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Andiuoli S., Dickinson T., Hickey E.K., Dougherty B.A., Morrison D., Salith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 745 LTPDIKKEILAF-----YHKHQVNILLNNDISYYTSNRLIKTEAHLSNINKLSQLNL 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                344 WIKOLNKRLEKFDSEIINCRVTSEQIS-CYKSDISYTVFLRYFIADF----VQEDKALYL 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       399 DCDLVVTKNLDDLFATDLODYPLAAVRDFGGRAYFGQEIFNAGVLLVNNAFWKKENMTQK 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   686 YQEEMDMLKDLKLIQNKDAKIAVSIFYPNTLNGLVKKLNNIIEYNKNIFVIILHVD-KNH 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232
                                                                                                                                                                                                                                                                                                                                         VSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIMS 494
                                                                                                                                                                                                                                                                                                                                                                                       495 KPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLK---EFLKDKTLACVYTINR 551
                                                                                                                                                                                                                                                                                                                                                                                                              QENAGLSAARNTGLNNMSGNYVTFVDSDDWIEQDYVETLYKKIVEYQADIAVGNYYSFNE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                      552 N------VNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHL-- 593
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7 ITVIVPVYNVENYLRKCLDSIITQTYKNIEIVVVNDGSIDASGEICKEFSEMDHRILYIE 66
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 ALVDAMSERITLLANMGYPLEKHLAVYRQMLEVSLAN----GOASGLSDTATY----KE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----TDGFNENIENAVDYDMFLKLSEVGKFKHLNKICY-NRVLHGD------
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                                                                                                                                                                                                                                                                                            DB 16; Length 696;
                                                                                                                                                                                                                                                                                          5.3%; Score 268.5; DB 16; Length
20.5%; Pred. No. 3.3e-06;
tive 96; Mismatches 181; Indels
                                                                                                                                                                                                           InterPro; JET/17; Glycos_transf_2.
InterPro; IPR001173; Glycos_transf_2.
InterPro; IPR002495; GT_8.
Pfam; PF01551; Glycos_transf_2; 1.
Pfam; PF01501; Glyco_transf_8; 1.
SEQUENCE 696 AA; 81336 MW; ADCA9C01AABB32C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
spore coat polysaccharide biosynthesis protein.
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                                        MEDLINE=21357209; PubMed=11463916;
                                                                                                                                                                         Science 293:498-506(2001).
EMBL; AE007470; AAK75845.1; -.
TIGR; SP1771; -.
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Matches 101; Conservative
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                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  Query Match
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Q8XN34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRKYIFNKTAEYQEEMDMLKDLKLIQNKDAKIAVSIFYPNTLNGLVKKLNNIIEYNKNIF 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  735 VIILHVDKNHLTPDIKKEILAFYHKHQ------VNILLNNDISYYTSNRLIKTEAHLS 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 QENRGSSEARKGYEMSTGEFILFVDGDDWIRNDTIEVLLE-----YS----N 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 EIQK----IWSLLYDK----INNEKIELRDTQFLREILTNNISIN-----IWNKF----I 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        435 VSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIMS 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                          STRAIN-13 / TYPE A;
PubMed=11792842;
Shinizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shinizu T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      495 KPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDKTLACVYTTNRNVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               555 PDGSLIANGYNWPEFSREKLTTAMIAHHFRWFTIRAWHLTDGFNENIENAVDYDMFLKLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 VI------KEKLYFYFKRENSITSIISPKILETKDAMYFIKNILIE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             615 EVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVNQSLNRQGINYNYDKFDDLDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 16; Length 348;
Clostridium perfringens.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Clostridiales; Clostridiaceae; Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 NNKYFKKDEKNLDCYWRFFYLNAIN------NYYLGKILALIIK 331
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MEDLINE-21595285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto
                                                                                                                                                                                                                                                                                                                                                                                                       348 AA; 41769 MW; AE46C19FA8E52C93 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein Alr3067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae;
NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.2%; Score 265.5; DB 16;
23.3%; Pred. No. 2.1e-06;
tive 68; Mismatches 132;
                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002)
EMBL, AP003187; BAB80210.1;
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2: 1.
COmplete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sest Local Similarity 23.33
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                                                                                                                                   SEQUENCE FROM N.A.
                                                                               NCBI_TaxID=1502;
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                                                                                                                                                                                                                                                                                                                                    492 IMSKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVEL---CLKEFLKDKTLACVYT 548
                                                                                                                                                                                                                                                                                                                                                         127 YYKFANEADSYADESNSFAGDVYAELLIKNFLQNGSN-PLIRRAAIDSVGL------ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                              589 RAWHLTDGFNENIENAVDYDMFLKLSEVGKFKHLNK--ICYNRVLHGDNTSIKKLGIQKK 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NHFVVVNQSLNRQGINYYNYDKFDDLDESRKYIFNKTAE--YQEEMDMLKDLKLIQNKDA 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 YSSIVIERAFNAAPPQLQHLKK-----QSLAWVYKFTAQQCLKYNSHKLADIKLAA-KRL 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317,4331(2000).
EMBL: AP001519; BAB07432.1; --
InterPro: IPR001173; Glycos_transf_2.
Pfam: PF00535; Glycos_transf_2; 1.
                                                                                                                                                                                                                                        61; Gaps
                                                                                                                                                                                                                                                                                        10 VPIISVIIPVYNGEKTIIETIASVQHQTFLDIEIIVINDGSTDNTFELVRNIQDN--RLK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.,
                                                                                                                                                                                                       DB 16; Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 261.5; DB 16; Length 303;
Pred. No. 2.8e-06;
                                                            "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                       Query Match 5.2%; Score 264.5; DB 16; Length Best Local Similarity 25.4%; Pred. No. 2.1e-06; Matches 82; Conservative 64; Mismatches 116; Indels
                                                                                                      EMBL, AP003591, BAB74766.1; -.
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2.1.
Hypothetical protein; Complete proteome.
SEQUENCE 323 AA; 36955 MW; 0AA1437F8EC42D89 CRC64;
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Last annotation update)
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MEDLINE-20512582; Pubmed-11058132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1:::: | ::|| 280 KMAITLYPKNLLEDYTHGLIRKL 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transferase, Complete proteome. SEOURNCE 303 AA; 35235 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes;
Bacillaceae; Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus halodurans.
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Q9K6L6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 KPL----VRYYNYTTNKQISDDIKKYESAIEYIDNKYVDLYSKVSEEIRRKHRHSMTMLI 252
                                                        435 VSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIMS 494
                                                                                                                                                                           495 -KPNGGIASASNAAVSFAKGYYIGOLDSDDYLEPDAVELCLKEFLKDKTLACVYT---- 548
                                                                                                                                                                                                                                                                                                 ---TNRNVNPDGSLIANGYNWPE----FSREKL-----TTAMIAHHFRMFTIRAWHLTD 595
                                                                                                                                                                                                                                                                                                                                                                                                                     596 --GFNENIENAVDYDMFLKLSEVGRFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVN 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        654 QSLNRQGINYYNYDKFDDL-DESRKY-----IFNKTAE----YQEEMDMLK 694
Gaps
                                                                                                                61
                                                                                          95;
95; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ::|: |:|
253 VNKALRNQSPKVARAYLKNSFLKRPTLTAIIMYMLSFLKY
60; Mismatches
Conservative
90;
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